

HT 2260

SEQUENCE LISTING

74 ATTACHMENT

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PATENT & TRADEMARK OFFICE

(1) GENERAL INFORMATION:

Express Mail #EI18682182JUS

(i) APPLICANT:

(A) NAME: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

(ii) TITLE OF INVENTION: Protein/(Poly)peptide libraries

(iii) NUMBER OF SEQUENCES: 371

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: James F. Haley, Jr., Esq. c/o FISH & NEAVE
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) ZIP: 10020

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 95 11 3021.0
(B) FILING DATE: 18-AUG-1995

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: James F. Haley, Jr., Esq.
(B) REGISTRATION NUMBER: 27,794
(C) DOCKET NUMBER: MORPHO/5

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212)596-9000
(B) TELEFAX: (212)596-9090

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ala Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15
 Gly Gly Gly Ser
 20

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCAGCGGGTG GCGGTTCTGG CGGCGGTGGG AGCGGTGGCG GTGGTTCTGG CGGTGGTGGT 60
 TCCGATATCG GTCCACGTAC GG 82

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AATTCCGTAC GTGGACCGAT ATCGGAACCA CCACCGCCAG AACCACCGCC ACCGCTCCCA 60

CCGCCGCCAG AACCGCCACC CGC

83

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:28..45
- (D) OTHER INFORMATION:/product= "6 random codons by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATACGGCCG TGTATTATTG CGCGCGTNNK NNKNNKNNKN NKNNKGATTA TTGGGGCCAA

60

GGCACCCCTG

69

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:28..57
- (D) OTHER INFORMATION:/product= "10 random codons by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:58..60
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (TTT/ATG)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:64..66
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (GTT/TAT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

228

GATACGGCCG TGTATTATTG CGCGCGTNNK NNKNNKNNKN NKNNKNNKNN KNNKNNKWTk 60
 GATKWTGTTGGG GCCAAGGCAC CCTG 84

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATACGGCCG TGTATTATTG C 21

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGGTGCCT TGGCCCC 17

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCAGAAGGCG AACGTCC 17

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 39..41
- (D) OTHER INFORMATION: /product= "random codon (mixture of GCT, CGT, CAT, TCT, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 42..53
- (D) OTHER INFORMATION: /product= "random codons by trinucleotide mutagenesis (19 aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 57..59
- (D) OTHER INFORMATION: /product= "random codon by trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGGAAGCTGA AGACGTGGGC GTGTATTATT GCCAGCAGBV TNNKNNKNNK NNKCCGNNKT 60

TTGGCCAGGG TACGAAAGTT 80

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AACTTTCGTA CCCTGGCC 18

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:21..23
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

* (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:27..35
- (D) OTHER INFORMATION:/product= "random codons by trinucleotide mutagenesis (19 aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:36..41
- (D) OTHER INFORMATION:/product= "random codons by mixed monomers (A/G A/C/G T)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:42..44
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:48..50
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AGGGTCTCGA GTGGGTGAGC NNKAT'TNNKN NKNNKRVTRV TNNKACCNNK TATGCGGATA 60

GCGTGAAAGG CCGT'TTTACC AT'TTCACGTG ATAATTCGAA AAACACCA 108

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:21..23
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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- (B) LOCATION:27..32
- (D) OTHER INFORMATION:/product= "random codons by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:33..38
- (D) OTHER INFORMATION:/product= "random codons by mixed monomers (A/G A/C/G T)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:39..41
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:45..47
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGGGTCTCGA GTGGGTGAGC NNKATTNNKN NKRVTTRVTNN KACCNKKTAT GCGGATAGCG 60
 TGAAAGGCCG TTTTACCATT TCACGTGATA ATTGAAAAA CACCA 105

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGGTGTTTTT CGAATTATCA 20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

232

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 Arg

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10           15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
          20           25           30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
          50           55           60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65           70           75           80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asn Ser Pro
          85           90           95
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
          100          105

```

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1           5           10           15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
          20           25           30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
          35           40           45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
          50           55           60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

```

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65		70		75		80									
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
			85						90					95	
Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile
			100					105					110		
Lys	Arg														

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln
1				5					10					15	
Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Asn	Asn
			20					25					30		
Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu
			35				40					45			
Ile	Tyr	Asp	Asn	Asn	Lys	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser
		50				55					60				
Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln
65					70					75				80	
Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Thr	Trp	Asp	Asp	Ser	Leu
			85						90					95	
Ser	Gly	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln
			100					105					110		

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

235

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser
 85 90 95
 Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr
 1 5 10 15
 Ala Arg Ile Thr Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Ala Ser
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Asp
 35 40 45
 Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn
 50 55 60
 Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val Gln Ala Glu Asp
 65 70 75 80
 Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Ser Ser Gly Asn Val Val
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:

236

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1           5           10           15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20          25          30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35          40          45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50          55          60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65          70          75          80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Arg Ala Pro Gly Tyr Cys Ser Gly Phe Asp Tyr Trp Gly Gln Gly
100         105         110
Thr Leu Val Thr Val Ser Ser
115

```

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20          25          30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35          40          45
Gly Trp Ile Asn Pro Asn Ser Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50          55          60

```

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Gly Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Glx Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala His Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ile His Asn Ile Gly Glu Ala Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Ser Tyr Asp Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Gly Gly Ser Gly Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Gly Gly Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30
 Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60
 Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Asp Pro Gly Gly Phe Asp Val Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 amino acids

241

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1           5           10           15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
          20           25           30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
          35           40           45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
          50           55           60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His
          85           90           95
Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
          100          105          110
Arg Thr
  
```

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
          20           25           30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
          50           55           60
  
```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
 85 90 95
 Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110
 Lys Arg Thr
 115

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30
 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
 85 90 95
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr
 85 90 95
 Pro Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids

244

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1           5           10           15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20           25           30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35           40           45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50           55           60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65           70           75           80
Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Val
85           90           95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100           105

```

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1           5           10           15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20           25           30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35           40           45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50           55           60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65           70           75           80

```

245

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

246

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60
 Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser

247

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30
 Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
 35 40 45
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60
 Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..327
(D) OTHER INFORMATION: /product= "V kappa 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GAT ATC CAG ATG ACC CAG AGC CCG TCT AGC CTG AGC GCG AGC GTG GGT	48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly	
1 5 10 15	
GAT CGT GTG ACC ATT ACC TGC AGA GCG AGC CAG GGC ATT AGC AGC TAT	96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr	
20 25 30	
CTG GCG TGG TAC CAG CAG AAA CCA GGT AAA GCA CCG AAA CTA TTA ATT	144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile	
35 40 45	
TAT GCA GCC AGC AGC TTG CAA AGC GGG GTC CCG TCC CGT TTT AGC GGC	192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly	
50 55 60	
TCT GGA TCC GGC ACT GAT TTT ACC CTG ACC ATT AGC AGC CTG CAA CCT	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	
65 70 75 80	
GAA GAC TTT GCG ACC TAT TAT TGC CAG CAG CAT TAT ACC ACC CCG CCG	288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro	
85 90 95	
ACC TTT GGC CAG GGT ACG AAA GTT GAA ATT AAA CGT ACG	327
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr	
100 105	

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: /product= "V kappa 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAT ATC GTG ATG ACC CAG AGC CCA CTG AGC CTG CCA GTG ACT CCG GGC	48
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly	
110 115 120 125	
GAG CCT GCG AGC ATT AGC TGC AGA AGC AGC CAA AGC CTG CTG CAT AGC	96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
130 135 140	
AAC GGC TAT AAC TAT CTG GAT TGG TAC CTT CAA AAA CCA GGT CAA AGC	144
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
145 150 155	
CCG CAG CTA TTA ATT TAT CTG GGC AGC AAC CGT GCC AGT GGG GTC CCG	192
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro	
160 165 170	
GAT CGT TTT AGC GGC TCT GGA TCC GGC ACC GAT TTT ACC CTG AAA ATT	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
175 180 185	
AGC CGT GTG GAA GCT GAA GAC GTG GGC GTG TAT TAT TGC CAG CAG CAT	288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His	
190 195 200 205	
TAT ACC ACC CCG CCG ACC TTT GGC CAG GGT ACG AAA GTT GAA ATT AAA	336
Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
210 215 220	
CGT ACG	342

251

Arg Thr

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1             5             10             15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
          20             25             30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
          35             40             45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
          50             55             60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65             70             75             80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His
          85             90             95
Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
          100            105            110

```

Arg Thr

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: /product= "V kappa 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

GAT ATC GTG CTG ACC CAG AGC CCG GCG ACC CTG AGC CTG TCT CCG GGC
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
115             120             125             130

```

48

252

GAA CGT GCG ACC CTG AGC TGC AGA GCG AGC CAG AGC GTG AGC AGC AGC	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser	
135 140 145	
TAT CTG GCG TGG TAC CAG CAG AAA CCA GGT CAA GCA CCG CGT CTA TTA	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
150 155 160	
ATT TAT GGC GCG AGC AGC CGT GCA ACT GGG GTC CCG GCG CGT TTT AGC	192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser	
165 170 175	
GGC TCT GGA TCC GGC ACG GAT TTT ACC CTG ACC ATT AGC AGC CTG GAA	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu	
180 185 190	
CCT GAA GAC TTT GCG GTG TAT TAT TGC CAG CAG CAT TAT ACC ACC CCG	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro	
195 200 205 210	
CCG ACC TTT GGC CAG GGT ACG AAA GTT GAA ATT AAA CGT ACG	330
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr	
215 220	

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser	
20 25 30	
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser	
50 55 60	
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu	
65 70 75 80	
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro	
85 90 95	
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..345

(D) OTHER INFORMATION: /product= "V kappa 4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GAT ATC GTG ATG ACC CAG AGC CCG GAT AGC CTG GCG GTG AGC CTG GGC	48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
115 120 125	
GAA CGT GCG ACC ATT AAC TGC AGA AGC AGC CAG AGC GTG CTG TAT AGC	96
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser	
130 135 140	
AGC AAC AAC AAA AAC TAT CTG GCG TGG TAC CAG CAG AAA CCA GGT CAG	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
145 150 155	
CCG CCG AAA CTA TTA ATT TAT TGG GCA TCC ACC CGT GAA AGC GGG GTC	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
160 165 170	
CCG GAT CGT TTT AGC GGC TCT GGA TCC GGC ACT GAT TTT ACC CTG ACC	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
175 180 185 190	
ATT TCG TCC CTG CAA GCT GAA GAC GTG GCG GTG TAT TAT TGC CAG CAG	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
195 200 205	
CAT TAT ACC ACC CCG CCG ACC TTT GGC CAG GGT ACG AAA GTT GAA ATT	336
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
210 215 220	
AAA CGT ACG	345
Lys Arg Thr	
225	

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

254

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys Arg Thr
 115

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..327
- (D) OTHER INFORMATION: /product= "V lambda 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CAG AGC GTG CTG ACC CAG CCG CCT TCA GTG AGT GGC GCA CCA GGT CAG	48
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln	
120 125 130	
CGT GTG ACC ATC TCG TGT AGC GGC AGC AGC AGC AAC ATT GGC AGC AAC	96
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn	
135 140 145	
TAT GTG AGC TGG TAC CAG CAG TTG CCC GGG ACG GCG CCG AAA CTG CTG	144
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu	
150 155 160	
ATT TAT GAT AAC AAC CAG CGT CCC TCA GGC GTG CCG GAT CGT TTT AGC	192
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser	
165 170 175	
GGA TCC AAA AGC GGC ACC AGC GCG AGC CTT GCG ATT ACG GGC CTG CAA	240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln	
180 185 190 195	
AGC GAA GAC GAA GCG GAT TAT TAT TGC CAG CAG CAT TAT ACC ACC CCG	288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro	
200 205 210	

CCT GTG TTT GGC GGC GGC ACG AAG TTA ACC GTT CTT GGC
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 215 220

327

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30
 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
 85 90 95
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: /product= "V lambda 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

CAG AGC GCA CTG ACC CAG CCA GCT TCA GTG AGC GGC TCA CCA GGT CAG
 Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 110 115 120 125
 AGC ATT ACC ATC TCG TGT ACG GGT ACT AGC AGC GAT GTG GGC GGC TAT

48

96

256

Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr		
				130					135					140			
AAC	TAT	GTG	AGC	TGG	TAC	CAG	CAG	CAT	CCC	GGG	AAG	GCG	CCG	AAA	CTG	144	
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu		
			145					150					155				
ATG	ATT	TAT	GAT	GTG	AGC	AAC	CGT	CCC	TCA	GGC	GTG	AGC	AAC	CGT	TTT	192	
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe		
		160					165					170					
AGC	GGA	TCC	AAA	AGC	GGC	AAC	ACC	GCG	AGC	CTG	ACC	ATT	AGC	GGC	CTG	240	
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu		
	175					180					185						
CAA	GCG	GAA	GAC	GAA	GCG	GAT	TAT	TAT	TGC	CAG	CAG	CAT	TAT	ACC	ACC	288	
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr		
	190				195				200						205		
CCG	CCT	GTG	TTT	GGC	GGC	GGC	ACG	AAG	TTA	ACC	GTT	CTT	GGC			330	
Pro	Pro	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly				
			210					215									

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Gln	Ser	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln		
1				5					10					15			
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr		
			20					25					30				
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu		
		35				40						45					
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe		
	50					55					60						
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu		
	65				70					75					80		
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr		
			85					90						95			
Pro	Pro	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly				
		100					105						110				

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..321

(D) OTHER INFORMATION: /product= "V lambda 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AGC TAT GAA CTG ACC CAG CCG CCT TCA GTG AGC GTT GCA CCA GGT CAG	48
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln	
115 120 125	
ACC GCG CGT ATC TCG TGT AGC GGC GAT GCG CTG GGC GAT AAA TAC GCG	96
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala	
130 135 140	
AGC TGG TAC CAG CAG AAA CCC GGG CAG GCG CCA GTT CTG GTG ATT TAT	144
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr	
145 150 155	
GAT GAT TCT GAC CGT CCC TCA GGC ATC CCG GAA CGC TTT AGC GGA TCC	192
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser	
160 165 170	
AAC AGC GGC AAC ACC GCG ACC CTG ACC ATT AGC GGC ACT CAG GCG GAA	240
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu	
175 180 185 190	
GAC GAA GCG GAT TAT TAT TGC CAG CAG CAT TAT ACC ACC CCG CCT GTG	288
Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Val	
195 200 205	
TTT GGC GGC GGC ACG AAG TTA ACC GTT CTT GGC	321
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly	
210 215	

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln	
1 5 10 15	
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala	
20 25 30	
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr	
35 40 45	
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser	

50		55		60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu				
65		70		75
Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Val				
	85		90	95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly				
	100		105	

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: /product= "VH1A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CAG GTG CAA TTG GTT CAG TCT GGC GCG GAA GTG AAA AAA CCG GGC AGC	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser	
110 115 120	
AGC GTG AAA GTG AGC TGC AAA GCC TCC GGA GGC ACT TTT AGC AGC TAT	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr	
125 130 135	
GCG ATT AGC TGG GTG CGC CAA GCC CCT GGG CAG GGT CTC GAG TGG ATG	144
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
140 145 150 155	
GGC GGC ATT ATT CCG ATT TTT GGC ACG GCG AAC TAC GCG CAG AAG TTT	192
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe	
160 165 170	
CAG GGC CGG GTG ACC ATT ACC GCG GAT GAA AGC ACC AGC ACC GCG TAT	240
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr	
175 180 185	
ATG GAA CTG AGC AGC CTG CGT AGC GAA GAT ACG GCC GTG TAT TAT TGC	288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	
190 195 200	
GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA	336
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln	
205 210 215	
GGC ACC CTG GTG ACG GTT AGC TCA G	361
Gly Thr Leu Val Thr Val Ser Ser	
220 225	

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1           5           10           15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20           25           30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35           40           45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50           55           60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
          65           70           75           80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
          100          105          110
Gly Thr Leu Val Thr Val Ser Ser
          115          120

```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: /product= "VH1B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

CAG GTG CAA TTG GTT CAG AGC GGC GCG GAA GTG AAA AAA CCG GGC GCG      48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
          125          130          135
AGC GTG AAA GTG AGC TGC AAA GCC TCC GGA TAT ACC TTT ACC AGC TAT      96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

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260

140										145					150					
TAT	ATG	CAC	TGG	GTC	CGC	CAA	GCC	CCT	GGG	CAG	GGT	CTC	GAG	TGG	ATG	144				
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met					
		155					160					165								
GGC	TGG	ATT	AAC	CCG	AAT	AGC	GGC	GGC	ACG	AAC	TAC	GCG	CAG	AAG	TTT	192				
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe					
	170					175					180									
CAG	GGC	CGG	GTG	ACC	ATG	ACC	CGT	GAT	ACC	AGC	ATT	AGC	ACC	GCG	TAT	240				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr					
185					190					195					200					
ATG	GAA	CTG	AGC	AGC	CTG	CGT	AGC	GAA	GAT	ACG	GCC	GTG	TAT	TAT	TGC	288				
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys					
				205					210					215						
GCG	CGT	TGG	GGC	GGC	GAT	GGC	TTT	TAT	GCG	ATG	GAT	TAT	TGG	GGC	CAA	336				
Ala	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln					
			220				225						230							
GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	G								361				
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser													
		235					240													

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	
		20					25					30				
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35				40						45				
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	
	50					55					60					
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr	
65					70				75					80		
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90						95		
Ala	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	
		100					105					110				
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		115				120										

(2) INFORMATION FOR SEQ ID NO: 60:

261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: /product= "VH2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CAG GTG CAA TTG AAA GAA AGC GGC CCG GCC CTG GTG AAA CCG ACC CAA	48
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln	
125 130 135	
ACC CTG ACC CTG ACC TGT ACC TTT TCC GGA TTT AGC CTG TCC ACG TCT	96
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser	
140 145 150	
GGC GTT GGC GTG GGC TGG ATT CGC CAG CCG CCT GGG AAA GCC CTC GAG	144
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu	
155 160 165	
TGG CTG GCT CTG ATT GAT TGG GAT GAT GAT AAG TAT TAT AGC ACC AGC	192
Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser	
170 175 180	
CTG AAA ACG CGT CTG ACC ATT AGC AAA GAT ACT TCG AAA AAT CAG GTG	240
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val	
185 190 195 200	
GTG CTG ACT ATG ACC AAC ATG GAC CCG GTG GAT ACG GCC ACC TAT TAT	288
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr	
205 210 215	
TGC GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC	336
Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly	
220 225 230	
CAA GGC ACC CTG GTG ACG GTT AGC TCA G	364
Gln Gly Thr Leu Val Thr Val Ser Ser	
235 240	

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

262

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60
 Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: /product= "VH3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAA GTG CAA TTG GTG GAA AGC GGC GGC GGC CTG GTG CAA CCG GGC GGC	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
125 130 135	
AGC CTG CGT CTG AGC TGC GCG GCC TCC GGA TTT ACC TTT AGC AGC TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
140 145 150	
GCG ATG AGC TGG GTG CGC CAA GCC CCT GGG AAG GGT CTC GAG TGG GTG	144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
155 160 165	
AGC GCG ATT AGC GGT AGC GGC GGC AGC ACC TAT TAT GCG GAT AGC GTG	192
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val	
170 175 180 185	
AAA GGC CGT TTT ACC ATT TCA CGT GAT AAT TCG AAA AAC ACC CTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	

263

190	195	200	
CTG CAA ATG AAC AGC CTG CGT GCG GAA GAT ACG GCC GTG TAT TAT TGC			288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
205	210	215	
GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA			336
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln			
220	225	230	
GGC ACC CTG GTG ACG GTT AGC TCA G			361
Gly Thr Leu Val Thr Val Ser Ser			
235	240		

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr			
20	25	30	
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln			
100	105	110	
Gly Thr Leu Val Thr Val Ser Ser			
115	120		

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

264

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..357
 (D) OTHER INFORMATION: /product= "VH4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CAG GTG CAA TTG CAA GAA AGT GGT CCG GGC CTG GTG AAA CCG AGC GAA	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu	
125 130 135	
ACC CTG AGC CTG ACC TGC ACC GTT TCC GGA GGC AGC ATT AGC AGC TAT	96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr	
140 145 150	
TAT TGG AGC TGG ATT CGC CAG CCG CCT GGG AAG GGT CTC GAG TGG ATT	144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile	
155 160 165	
GGC TAT ATT TAT TAT AGC GGC AGC ACC AAC TAT AAT CCG AGC CTG AAA	192
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys	
170 175 180	
AGC CGG GTG ACC ATT AGC GTT GAT ACT TCG AAA AAC CAG TTT AGC CTG	240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu	
185 190 195 200	
AAA CTG AGC AGC GTG ACG GCG GCG GAT ACG GCC GTG TAT TAT TGC GCG	288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala	
205 210 215	
CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA GGC	336
Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly	
220 225 230	
ACC CTG GTG ACG GTT AGC TCA G	358
Thr Leu Val Thr Val Ser Ser	
235	

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu	
1 5 10 15	
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr	
20 25 30	
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile	
35 40 45	
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys	
50 55 60	

265

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: /product= "VH5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAA GTG CAA TTG GTT CAG AGC GGC GCG GAA GTG AAA AAA CCG GGC GAA	48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu	
120 125 130 135	
AGC CTG AAA ATT AGC TGC AAA GGT TCC GGA TAT TCC TTT ACG AGC TAT	96
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr	
140 145 150	
TGG ATT GGC TGG GTG CGC CAG ATG CCT GGG AAG GGT CTC GAG TGG ATG	144
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met	
155 160 165	
GGC ATT ATT TAT CCG GGC GAT AGC GAT ACC CGT TAT TCT CCG AGC TTT	192
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe	
170 175 180	
CAG GGC CAG GTG ACC ATT AGC GCG GAT AAA AGC ATT AGC ACC GCG TAT	240
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr	
185 190 195	
CTT CAA TGG AGC AGC CTG AAA GCG AGC GAT ACG GCC ATG TAT TAT TGC	288
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys	
200 205 210 215	
GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA	336
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln	
220 225 230	
GGC ACC CTG GTG ACG GTT AGC TCA G	361
Gly Thr Leu Val Thr Val Ser Ser	

266

235

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1             5             10             15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
      20             25             30
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
      35             40             45
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
      50             55             60
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
      65             70             75             80
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
      85             90             95
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
      100             105             110
Gly Thr Leu Val Thr Val Ser Ser
      115             120

```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369
- (D) OTHER INFORMATION: /product= "VH6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

CAG GTG CAA TTG CAA CAG TCT GGT CCG GGC CTG GTG AAA CCG AGC CAA
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
      125             130             135
ACC CTG AGC CTG ACC TGT GCG ATT TCC GGA GAT AGC GTG AGC AGC AAC

```

48

96

267

Thr	Leu	Ser	Leu	Thr	Cys	Ala	Ile	Ser	Gly	Asp	Ser	Val	Ser	Ser	Asn	
			140					145					150			
AGC	GCG	GCG	TGG	AAC	TGG	ATT	CGC	CAG	TCT	CCT	GGG	CGT	GGC	CTC	GAG	144
Ser	Ala	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Arg	Gly	Leu	Glu	
		155					160					165				
TGG	CTG	GGC	CGT	ACC	TAT	TAT	CGT	AGC	AAA	TGG	TAT	AAC	GAT	TAT	GCG	192
Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn	Asp	Tyr	Ala	
	170					175					180					
GTG	AGC	GTG	AAA	AGC	CGG	ATT	ACC	ATC	AAC	CCG	GAT	ACT	TCG	AAA	AAC	240
Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Asn	Pro	Asp	Thr	Ser	Lys	Asn	
185					190					195					200	
CAG	TTT	AGC	CTG	CAA	CTG	AAC	AGC	GTG	ACC	CCG	GAA	GAT	ACG	GCC	GTG	288
Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Glu	Asp	Thr	Ala	Val	
			205					210						215		
TAT	TAT	TGC	GCG	CGT	TGG	GGC	GGC	GAT	GGC	TTT	TAT	GCG	ATG	GAT	TAT	336
Tyr	Tyr	Cys	Ala	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	
		220				225						230				
TGG	GGC	CAA	GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	G					370
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
	235					240										

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln	
1				5				10						15		
Thr	Leu	Ser	Leu	Thr	Cys	Ala	Ile	Ser	Gly	Asp	Ser	Val	Ser	Ser	Asn	
			20					25					30			
Ser	Ala	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Arg	Gly	Leu	Glu	
		35				40						45				
Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn	Asp	Tyr	Ala	
	50				55						60					
Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Asn	Pro	Asp	Thr	Ser	Lys	Asn	
65				70				75							80	
Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Glu	Asp	Thr	Ala	Val	
			85					90						95		
Tyr	Tyr	Cys	Ala	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	
		100				105						110				
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
	115					120										

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GAATGCATAC GCTGATATCC AGATGACCCA GAGCCCGTCT AGCCTGAGC

49

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CGCTCTGCAG GTAATGGTCA CACGATCACC CACGCTCGCG CTCAGGCTAG ACGGGC

56

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GACCATTACC TGCAGAGCGA GCCAGGGCAT TAGCAGCTAT CTGGCGTGGT ACCAGCAG

58

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

269

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CTTTGCAAGC TGCTGGCTGC ATAAATTAAT AGTTTCGGTG CTTTACCTGG TTTCTGCTGG 60
TACCACGCCA G 71

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CAGCCAGCAG CTTGCAAAGC GGGGTCCCGT CCCGTTTTAG CGGCTCTGGA TCCGGCACTG 60
ATTTTAC 67

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GATAATAGGT CGCAAAGTCT TCAGGTTGCA GGCTGCTAAT GGTCAGGGTA AAATCAGTGC 60
CGGATCC 67

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGATATCGTG ATGACCCAGA GCCCACTGAG CCTGCCAGTG ACTCCGGGCG AGCC

54

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CCCGTTGCTA TGCAGCAGGC TTTGGCTGCT TCTGCAGCTA ATGCTCGCAG GCTCGCCCGG

60

AGTCAC

66

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CTGCTGCATA GCAACGGCTA TAACTATCTG GATTGGTACC TTCAAAAACC AGGTCAAAGC

60

CC

62

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CGATCCGGGA CCCCACTGGC ACGGTTGCTG CCCAGATAAA TTAATAGCTG CGGGCTTTGA 60
 CCTGGTTTTT G 71

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

AGTGGGGTCC CGGATCGTTT TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT 60
 AGCCGTGTG 69

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCATGCAATA ATACAGCCC ACGTCTTCAG CTTCACACG GCTAATTTTC AGGG 54

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

GAATGCATAC GCTGATATCG TGCTGACCCA GAGCCCGG 38

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGCTCTGCAG CTCAGGGTCG CACGTTGCC CGGAGACAGG CTCAGGGTCG CCGGGCTCTG 60
 GGTCAGC 67

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCCTGAGCTG CAGAGCGAGC CAGAGCGTGA GCAGCAGCTA TCTGGCGTGG TACCAG 56

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GCACGGCTGC TCGCGCCATA AATTAATAGA CGCGGTGCTT GACCTGGTTT CTGCTGGTAC 60
 CAGCCAGAT AG 72

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GCGCGAGCAG CCGTGCAACT GGGGTCCCGG CGCGTTTTAG CGGCTCTGGA TCCGGCACGG 60
 ATTTTAC 67

- (2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GATAATACAC CGCAAAGTCT TCAGGTTCCA GGCTGCTAAT GGTCAGGGTA AAATCCGTGC 60
 CGGATC 66

- (2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GAATGCATAC GCTGATATCG TGATGACCCA GAGCCCGGAT AGCCTGGCG 49

- (2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

274

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GCTTCTGCAG TTAATGGTCG CACGTTGCC CAGGCTCACC GCCAGGCTAT CCGGGC

56

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CGACCATTAA CTGCAGAAGC AGCCAGAGCG TGCTGTATAG CAGCAACAAC AAAA ACTATC

60

TGGCGTGGTA CCAAG

74

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GATGCCCAAT AAATTAATAG TTTCGGCGGC TGACCTGGTT TCTGCTGGTA CCACGCCAGA

60

TAG

63

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AAACTATTAA TTTATTGGGC ATCCACCCGT GAAAGCGGGG TCCCGGATCG TTTTAGCGGC 60
TCTGGATCCG GCAC 74

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GATAATACAC CGCCACGTCT TCAGCTTGCA GGGACGAAAT GGTCAGGGTA AAATCAGTGC 60
CGGATCCAGA GCC 73

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GAATGCATAC GCTCAGAGCG TGCTGACCCA GCCGCCTTCA GTGAGTGG 48

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

276

CAATGTTGCT GCTGCTGCCG CTACACGAGA TGGTCACACG CTGACCTGGT GCGCCACTCA 60
 CTGAAGGCGG C 71

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GGCAGCAGCA GCAACATTGG CAGCAACTAT GTGAGCTGGT ACCAGCAGTT GCCCGGGAC 59

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGGCACGCC TGAGGGACGC TGGTTGTTAT CATAAATCAG CAGTTTCGGC GCCGTCCCGG 60
 GCAACTGC 68

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCCTCAGGCG TGCCGGATCG TTTTAGCGGA TCCTAAAAGCG GCACCAAGCGC GAGCCTTGCG 60

(2) INFORMATION FOR SEQ ID NO: 99:

277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGCTTCGTC TTCGCTTTGC AGGCCCGTAA TCGCAAGGCT CGCGCTGG

48

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

GAATGCATAC GCTCAGAGCG CACTGACCCA GCCAGCTTCA GTGAGCGGC

49

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CGCTGCTAGT ACCCGTACAC GAGATGGTAA TGCTCTGACC TGGTGAGCCG CTCACTGAAG

60

CTGG

64

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

278

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

GTACGGGTAC TAGCAGCGAT GTGGGCGGCT ATAACATGT GAGCTGGTAC CAGCAGCATC 60
CCGG 64

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CGCCTGAGGG ACGGTTGCTC ACATCATAAA TCATCAGTTT CGGCGCCTTC CCGGGATGCT 60
GCTGGTAC 68

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CAACCGTCCC TCAGGCGTGA GCAACCGTTT TAGCGGATCC AAAAGCGGCA ACACCGCGAG 60
CC 62

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGCTTCGTC TTCCGCTTGC AGGCCGCTAA TGGTCAGGCT CGCGGTGTTG CCG

53

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GAATGCATAC GCTAGCTATG AACTGACCCA GCCGCCTTCA GTGAGCG

47

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CGCCCAGCGC ATCGCCGCTA CACGAGATAC GCGCGGTCTG ACCTGGTGCA ACGCTCACTG

60

AAGGCGGC

68

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

288

GGCGATGCGC TGGGCGATAA ATACGCGAGC TGGTACCAGC AGAAACCCGG GCAGGCGC

58

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GCGTTCCGGG ATGCCTGAGG GACGGTCAGA ATCATCATAA ATCACCAGAA CTGGCGCCTG

60

CCCGGGTTTC

70

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

CAGGCATCCC GGAACGCTTT AGCGGATCCA ACAGCGGCAA CACCGCGACC CTGACCATTA

60

GCGG

64

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGCTTCGTC TTCCGCCTGA GTGCCGCTAA TGGTCAGGGT C

41

(2) INFORMATION FOR SEQ ID NO: 112:

281

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GCTCTTCACC CCTGTTACCA AAGCCCAGGT GCAATTG

37

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

GGCTTTGCAG CTCACCTTTCA CGCTGCTGCC CGGTTTTTTTC ACTTCCGCGC CAGACTGAAC
CAATTGCACC TGGGCTTTG

60

79

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GAAAGTGAGC TGCAAAGCCT CCGGAGGCAC TTTTAGCAGC TATGCGATTA GCTGGGTGCG
CCAAGCCCCCT GGGCAGGGTC

60

80

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid

282

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCCCTGAAAC TTCTGCGCGT AGTTCGCCGT GCCAAAATC GGAATAATGC CGCCCATCCA 60
 CTCGAGACCC TGCCCAGGGG C 81

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GCGCAGAAAGT TTCAGGGCCG GGTGACCATT ACCGCGGATG AAAGCACCAG CACCGCGTAT 60
 ATGGAACTGA GCAGCCTGCG 80

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCGCGCAATA ATACACGGCC GTATCTTCGC TACGCAGGCT GCTCAGTTCC 50

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

213

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

GGCTTTGCAG CTCAC TTCA CGCTCGCGCC CGGTTTTTTC ACTTCCGCGC CGCTCTGAAC 60
CAATTGCACC TGGGCTTTG 79

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

GAAAGTGAGC TGCAAAGCCT CCGGATATAC CTTTACCAGC TATTATATGC ACTGGGTCCG 60
CCAAGCCCCCT GGCAGGGTC 80

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GCCCTGAAAC TTCTGCGCGT AGTTCGTGCC GCCGCTATTC GGGTTAATCC AGCCCATCCA 60
CTCGAGACCC TGCCCAGGGG C 81

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GCGCAGAAGT TTCAGGGCCG GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT 60
ATGGAAGTGA GCAGCCTGCG 80

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GGTACAGGTC AGGGTCAGGG TTTGGGTCGG TTTCACCAGG GCCGGGCCGC TTTCTTTCAA 60
TTGCACCTGG GCTTTG 76

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTGACCCTGA CCTGTACCTT TTCCGGATTT AGCCTGTCCA CGTCTGGCGT TGGCGTGGGC 60
TGGATTCGCC AGCCGCCTGG GAAAG 85

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GCCTTTTCAG GCTGGTGCTA TAATACTTAT CATCATCCCA ATCAATCAGA GCCAGCCACT 60

CGAGGGCTTT CCCAGGCGGC TGG 83

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GCACCAGCCT GAAAACGCGT CTGACCATTA GCAAAGATAC TTCGAAAAAT CAGGTGGTGC 60

TGACTATGAC CAACATGG 78

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GCGCGCAATA ATAGGTGGCC GTATCCACCG GGTCCATGTT GGTCATAGTC AGC 53

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

CGAAGTGCAA TTGGTGAAA GCGGCGGCGG CCTGGTGCAA CCGGGCGGCA G 51

286

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CATAGCTGCT AAAGGTAAAT CCGGAGGCCG CGCAGCTCAG ACGCAGGCTG CCGCCCCGTT 60
GCAC 64

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GATTTACCTT TAGCAGCTAT GCGATGAGCT GGGTGCGCCA AGCCCCTGGG AAGGGTCTCG 60
AGTGGGTGAG 70

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

GGCCTTTTAC GCTATCCGCA TAATAGGTGC TGCCGCCGCT ACCGCTAATC GCGCTCACCC 60
ACTCGAGACC C 71

(2) INFORMATION FOR SEQ ID NO: 131:

287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CGGATAGCGT GAAAGGCCGT TTTACCATTT CACGTGATAA TTCGAAAAAC ACCCTGTATC 60
 TGCAAATGAA CAG 73

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CACGCGCGCA ATAATACACG GCCGTATCTT CCGCACGCAG GCTGTTTCATT TGCAGATACA 60
 GG 62

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

GGTCAGGCTC AGGGTTTCGC TCGGTTTCAC CAGGCCCGGA CCACTTTCTT GCAATTGCAC 60
 CTGGGCTTTG 70

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

288

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

GAAACCCTGA GCCTGACCTG CACCGTTTCC GGAGGCAGCA TTAGCAGCTA TTATTGGAGC 60

TGGATTGCGC AGCCGC 76

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

GATTATAGTT GGTGCTGCCG CTATAATAAA TATAGCCAAT CCACTCGAGA CCCTTCCCAG 60

GCGGCTGGCG AATCCAG 77

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CGGCAGCACC AACTATAATC CGAGCCTGAA AAGCCGGGTG ACCATTAGCG TTGATACTTC 60

GAAAAACCAG TTTAGCCTG 79

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid

289

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GCGCGCAATA ATACACGGCC GTATCCGCCG CCGTCACGCT GCTCAGTTTC AGGCTAAACT 60
GGTTTTTCG 69

- (2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

GCTCTTCACC CCTGTTACCA AAGCCGAAGT GCAATTG 37

- (2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CCTTTGCAGC TAATTTTCAG GCTTTCGCCG GGTTTTTTTCA CTTCCGCGCC GCTCTGAACC 60
AATTGCACTT CGGCTTTGG 79

- (2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CCTGAAAATT AGCTGCAAAG GTTCCGGATA TTCCTTTACG AGCTATTGGA TTGGCTGGGT 60
GCGCCAGATG CCTGG 75

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

CGGAGAATAA CGGGTATCGC TATCGCCCGG ATAAATAATG CCCATCCACT CGAGACCCTT 60
CCCAGGCATC TGGCGCAC 78

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CGATACCCGT TATTCTCCGA GCTTTCAGGG CCAGGTGACC ATTAGCGCGG ATAAAAGCAT 60
TAGCACCGCG TATCTTC 77

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GCGCGCAATA ATACATGGCC GTATCGCTCG CTTTCAGGCT GCTCCATTGA AGATACGCGG 60
TGCTAATG 68

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

GAAATCGCAC AGGTCAGGCT CAGGGTTTGG CTCGGTTTCA CCAGGCCCGG ACCAGACTGT 60
TGCAATTGCA CCTGGGCTTT G 81

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GCCTGACCTG TGCGATTTCC GGAGATAGCG TGAGCAGCAA CAGCGCGGCG TGGAAGTGA 60
TTCGCCAGTC TCCTGGGCG 79

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CACCGCATAA TCGTTATACC ATTTGCTACG ATAATAGGTA CGGCCCAGCC ACTCGAGGCC 60
ACGCCCAGGA GACTGGCG 78

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GGTATAACGA TTATGCGGTG AGCGTGAAAA GCCGGATTAC CATCAACCCG GATACTTCGA 60
AAAACCAAGTT TAGCCTGC 78

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

GCGCGCAATA ATACACGGCC GTATCTTCCG GGGTCACGCT GTTCAGTTGC AGGCTAAACT 60
GGTTTTTC 68

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

293

GGCTGAAGAC GTGGGCGTGT ATTATTGCCA GCAGCATTAT ACCACCCCGC CGACCTTTGG 60
 CCAGGGTAC 69

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

GCGGAAAAAT AAACACGCTC GGAGCAGCCA CCGTACGTTT AATTTCAACT TTCGTACCCT 60
 GGCCAAAGGT C 71

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GAGCGTGTTT ATTTTTCGCG CGAGCGATGA ACAACTGAAA AGCGGCACGG CGAGCGTGCT 60
 GTGCCTGCTG 70

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

CAGCGCGTTG TCTACTTTCC ACTGAACTTT CGCTTCACGC GGATAAAAGT TGTTTCAGCAG 60

294

GCACACCACG C

71

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GAAAGTAGAC AACGCGCTGC AAAGCGGCAA CAGCCAGGAA AGCGTGACCG AACAGGATAG 60

CAAAGATAG 69

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

GTTTTTCATA ATCCGCTTTG CTCAGGGTCA GGGTGCTGCT CAGAGAATAG GTGCTATCTT 60

TGCTATCCTG TTCG 74

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GCAAAGCGGA TTATGAAAAA CATAAAGTGT ATGCGTGCGA AGTGACCCAT CAAGGTCTGA 60

GCAGCCCGGT G 71

295

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

GGCATGCTTA TCAGGCCTCG CCACGATTAA AAGATTTAGT CACCGGGCTG CTCAGAC

57

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GGCGTCTAGA GGCCAAGGCA CCCTGGTGAC GGTTAGCTCA GCGTCGAC

48

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GTGCTTTTGC TGCTCGGAGC CAGCGGAAAC ACGCTTGGAC CTTTGGTCGA CGCTGAGCTA

60

ACC

63

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid

296

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CTCCGAGCAG CAAAAGCACC AGCGGCGGCA CGGCTGCCCT GGGCTGCCTG GTTAAAGATT 60
ATTTCC 66

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CTGGTCAGCG CCCCCTGTT CCAGCTCACG GTGACTGGTT CCGGGAATA ATCTTTAACC 60
AGGCA 65

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AGCGGGGCGC TGACCAGCGG CGTGCATACC TTTCCGGCGG TGCTGCAAAG CAGCGGCCTG 60

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

297

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GTGCCTAAGC TGCTGCTCGG CACGGTCACA ACGCTGCTCA GGTATACAG GCCGCTGCTT 60
 TGCAG 65

- (2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GAGCAGCAGC TTAGGCACTC AGACCTATAT TTGCAACGTG AACCATAAAC CGAGCAACAC 60
 C 61

- (2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCGCGAATTC GCTTTTCGGT TCCACTTTTT TATCCACTTT GGTGTTGCTC GGTTTATGG 59

- (2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic gene"

298

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 7..321
 (D) OTHER INFORMATION: /product= "C kappa"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CGTACG GTG GCT GCT CCG AGC GTG TTT ATT TTT CCG CCG AGC GAT GAA	48
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu	
125 130 135	
CAA CTG AAA AGC GGC ACG GCG AGC GTG GTG TGC CTG CTG AAC AAC TTT	96
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe	
140 145 150	
TAT CCG CGT GAA GCG AAA GTT CAG TGG AAA GTA GAC AAC GCG CTG CAA	144
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln	
155 160 165	
AGC GGC AAC AGC CAG GAA AGC GTG ACC GAA CAG GAT AGC AAA GAT AGC	192
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser	
170 175 180 185	
ACC TAT TCT CTG AGC AGC ACC CTG ACC CTG AGC AAA GCG GAT TAT GAA	240
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu	
190 195 200	
AAA CAT AAA GTG TAT GCG TGC GAA GTG ACC CAT CAA GGT CTG AGC AGC	288
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser	
205 210 215	
CCG GTG ACT AAA TCT TTT AAT CGT GGC GAG GCC TGATAAGCAT GC	333
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ala	
220 225	

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu	
1 5 10 15	
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro	
20 25 30	
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly	
35 40 45	
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr	
50 55 60	
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His	
65 70 75 80	

299

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
 85 90 95

Thr Lys Ser Phe Asn Arg Gly Glu Ala
 100 105

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..317
- (D) OTHER INFORMATION: /product= "CH1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

GCTCA GCG TCG ACC AAA GGT CCA AGC GTG TTT CCG CTG GCT CCG AGC	47
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
110 115	
AGC AAA AGC ACC AGC GGC GGC ACG GCT GCC CTG GGC TGC CTG GTT AAA	95
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
120 125 130 135	
GAT TAT TTC CCG GAA CCA GTC ACC GTG AGC TGG AAC AGC GGG GCG CTG	143
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
140 145 150	
ACC AGC GGC GTG CAT ACC TTT CCG GCG GTG CTG CAA AGC AGC GGC CTG	191
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
155 160 165	
TAT AGC CTG AGC AGC GTT GTG ACC GTG CCG AGC AGC AGC TTA GGC ACT	239
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
170 175 180	
CAG ACC TAT ATT TGC AAC GTG AAC CAT AAA CCG AGC AAC ACC AAA GTG	287
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
185 190 195	
GAT AAA AAA GTG GAA CCG AAA AGC GAA TTC TGATAAGCTT	327
Asp Lys Lys Val Glu Pro Lys Ser Glu Phe	
200 205	

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

300

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1				5					10					15	
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65					70					75					80
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85						90					95	
Lys	Val	Glu	Pro	Lys	Ser	Glu	Phe								
															100

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 85..396
- (D) OTHER INFORMATION: /product= "C lambda"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

GAAGACGAAG	CGGATTATTA	TTGCCAGCAG	CATTATACCA	CCCCGCCTGT	GTTTGGCGGC	60
GGCACGAAGT	TAACCGTTCT	TGGC	CAG	CCG	AAA	111
		Gln	Pro	Lys	Ala	
			105		110	
CTG	TTT	CCG	CCG	AGC	AGC	159
Leu	Phe	Pro	Pro	Ser	Ser	
				Glu	Glu	125
				Leu	Gln	
				Ala	Asn	
				Lys	Ala	
				Thr	Leu	
GTG	TGC	CTG	ATT	AGC	GAC	207
Val	Cys	Leu	Ile	Ser	Asp	
				Phe	Tyr	
				Pro	Gly	145
				Ala	Val	
				Thr	Val	
				Ala	Trp	
AAG	GCA	GAT	AGC	AGC	CCC	255
Lys	Ala	Asp	Ser	Ser	Pro	
				Val	Lys	
				Ala	Gly	160
				Val	Glu	
				Thr	Thr	
				Thr	Pro	

301

TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAT CTG AGC CTG	303
Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu	
165 170 175	
ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG	351
Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr	
180 185 190	
CAT GAG GGG AGC ACC GTG GAA AAA ACC GTT GCG CCG ACT GAG GCC	396
His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Ala	
195 200 205	
TGATAAGCAT GC	408

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
 1 5 10 15

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 20 25 30

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
 35 40 45

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
 50 55 60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 65 70 75 80

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 85 90 95

Lys Thr Val Ala Pro Thr Glu Ala
 100

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

302

GAAGACAAGC GGATTATTAT TGCCAGCAGC ATTATACCAC CCCGCCTGTG TTGGCGGCG 60
GCACGAAGTT AACCGTTC 78

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CAATTCTTCG CTGCTCGGCG GAAACAGCGT CACACTCGGT GCGGCTTTCG GCTGGCCAAG 60
AACGGTTAAC TTCGTGCCGC 80

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCCGAGCAG CGAAGAATTG CAGGCGAACA AAGCGACCCT GGTGTGCCTG ATTAGCGACT 60
TTTATCCGGG AGCCGTGACA 80

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

TGTTTGGAGG GTGTGGTGGT CTCCACTCCC GCCTTGACGG GGCTGCTATC TGCCTTCCAG 60

303

GCCACTGTCA CGGCTCCCGG

80

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

CCACACCCTC CAAACAAAGC AACAAACAAGT ACGCGGCCAG CAGCTATCTG AGCCTGACGC 60
 CTGAGCAGTG GAAGTCCCAC AGAAGCTACA GCTG 94

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

GCATGCTTAT CAGGCCTCAG TCGGCGCAAC GGTTTTTTCC ACGGTGCTCC CCTCATGCGT 60
 GACCTGGCAG CTGTAGCTTC 80

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..843
- (D) OTHER INFORMATION: /product= "VH3-Vk2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

304

ATG Met 105	AAA Lys	CAA Gln	AGC Ser	ACT Thr	ATT Ile 110	GCA Ala	CTG Leu	GCA Ala	CTC Leu	TTA Leu 115	CCG Pro	TTG Leu	CTC Leu	TTC Phe	ACC Thr 120	48
CCT Pro	GTT Val	ACC Thr	AAA Lys	GCC Ala 125	GAC Asp	TAC Tyr	AAA Lys	GAT Asp	GAA Glu 130	GTG Val	CAA Gln	TTG Leu	GTG Val	GAA Glu 135	AGC Ser	96
GGC Gly	GGC Gly	GGC Gly	CTG Leu 140	GTG Val	CAA Gln	CCG Pro	GGC Gly	GGC Gly	AGC Ser	CTG Leu 145	CGT Arg	CTG Leu	AGC Ser	TGC Cys	GCG Ala	144
GCC Ala	TCC Ser	GGA Gly 155	TTT Phe	ACC Thr	TTT Phe	AGC Ser	AGC Ser	TAT Tyr	GCG Ala	ATG Met	AGC Ser	TGG Trp 165	GTG Val	CGC Arg	CAA Gln	192
GCC Ala 170	CCT Pro	GGG Gly	AAG Lys	GGT Gly	CTC Leu	GAG Glu 175	TGG Trp	GTG Val	AGC Ser	GCG Ala 180	ATT Ile	AGC Ser	GGT Gly	AGC Ser	GGC Gly	240
GGC Gly 185	AGC Ser	ACC Thr	TAT Tyr	TAT Tyr	GCG Ala 190	GAT Asp	AGC Ser	GTG Val	AAA Lys	GGC Gly 195	CGT Arg	TTT Phe	ACC Thr	ATT Ile	TCA Ser 200	288
CGT Arg	GAT Asp	AAT Asn	TCG Ser	AAA Lys 205	AAC Asn	ACC Thr	CTG Leu	TAT Tyr	CTG Leu 210	CAA Gln	ATG Met	AAC Asn	AGC Ser	CTG Leu 215	CGT Arg	336
GCG Ala	GAA Glu	GAT Asp	ACG Thr 220	GCC Ala	GTG Val	TAT Tyr	TAT Tyr	TGC Cys 225	GCG Ala	CGT Arg	TGG Trp	GGC Gly	GGC Gly	GAT Asp 230	GGC Gly	384
TTT Phe	TAT Tyr 235	GCG Ala	ATG Met	GAT Asp	TAT Tyr	TGG Trp	GGC Gly 240	CAA Gln	GGC Gly	ACC Thr	CTG Leu	GTG Val	ACG Thr	GTT Val	AGC Ser	432
TCA Ser 250	GCG Ala	GGT Gly	GGC Gly	GGT Gly	TCT Ser	GGC Gly 255	GGC Gly	GGT Gly	GGG Gly	AGC Ser	GGT Gly 260	GGC Gly	GGT Gly	GGT Gly	TCT Ser	480
GGC Gly 265	GGT Gly	GGT Gly	GGT Gly	TCC Ser	GAT Asp 270	ATC Ile	GTG Val	ATG Met	ACC Thr	CAG Gln 275	AGC Ser	CCA Pro	CTG Leu	AGC Ser	CTG Leu 280	528
CCA Pro	GTG Val	ACT Thr	CCG Pro	GGC Gly 285	GAG Glu	CCT Pro	GCG Ala	AGC Ser	ATT Ile 290	AGC Ser	TGC Cys	AGA Arg	AGC Ser	AGC Ser	CAA Gln 295	576
AGC Ser	CTG Leu	CTG Leu	CAT His 300	AGC Ser	AAC Asn	GGC Gly	TAT Tyr	AAC Asn	TAT Tyr	CTG Leu	GAT Asp	TGG Trp	TAC Tyr	CTT Leu	CAA Gln	624
AAA Lys	CCA Pro	GGT Gly 315	CAA Gln	AGC Ser	CCG Pro	CAG Gln	CTA Leu 320	TTA Leu	ATT Ile	TAT Tyr	CTG Leu	GGC Gly 325	AGC Ser	AAC Asn	CGT Arg	672
GCC Ala 330	AGT Ser	GGG Gly	GTC Val	CCG Pro	GAT Asp	CGT Arg	TTT Phe	AGC Ser	GGC Gly	TCT Ser	GGA Gly	TCC Ser	GGC Gly	ACC Thr	GAT Asp	720
TTT Phe	ACC Thr	CTG Leu	AAA Lys	ATT Ile	AGC Ser	CGT Arg	GTG Val	GAA Glu	GCT Ala	GAA Glu	GAC Asp	GTG Val	GGC Gly	GTG Val	TAT Tyr	768

305

345		350		355		360	
TAT TGC CAG CAG CAT TAT ACC ACC CCG CCG ACC TTT GGC CAG GGT ACG							816
Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr							
		365		370		375	
AAA GTT GAA ATT AAA CGT ACG GAA TTC							843
Lys Val Glu Ile Lys Arg Thr Glu Phe							
		380		385			

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Met	Lys	Gln	Ser	Thr	Ile	Ala	Leu	Ala	Leu	Leu	Pro	Leu	Leu	Phe	Thr
1				5					10					15	
Pro	Val	Thr	Lys	Ala	Asp	Tyr	Lys	Asp	Glu	Val	Gln	Leu	Val	Glu	Ser
			20					25					30		
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala
		35					40					45			
Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Ser	Trp	Val	Arg	Gln
	50					55					60				
Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Ala	Ile	Ser	Gly	Ser	Gly
	65				70					75					80
Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser
			85						90					95	
Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg
			100					105					110		
Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Trp	Gly	Gly	Asp	Gly
		115					120					125			
Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
	130					135					140				
Ser	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	145				150					155					160
Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu
				165					170					175	
Pro	Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln
			180					185					190		
Ser	Leu	Leu	His	Ser	Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln
		195					200					205			
Lys	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg
	210					215					220				

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Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp
225 230 235 240

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
245 250 255

Tyr Cys Gln Gln His Tyr Thr Thr Pro Thr Phe Gly Gln Gly Thr
260 265 270

Lys Val Glu Ile Lys Arg Thr Glu Phe
275 280

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Cys Ala Arg Phe Gly Lys Met Asn Tyr Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Cys Ala Arg His Arg Thr Glu Trp His Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Cys Ala Arg Val Arg Glu Leu Tyr His Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Cys Ala Arg Lys Phe Leu Lys Ala Arg Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Cys Ala Arg Trp Asn Thr Thr Gly Tyr Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Cys Ala Arg Ile Asn Glu Ala Gln Pro Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Cys Ala Arg Thr Ala Ile Thr Arg Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Cys Ala Arg Trp Tyr Asn Arg Asn Ser Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Cys Ala Arg Ser Val Gly Asp Ser Lys Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Cys Ala Arg Ser Lys Thr Phe Ala Ala Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Cys Ala Arg Val Ala Pro Gln Tyr Asp Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Cys Ala Arg Met Gln Ser Glu Trp Met Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Cys Ala Arg Tyr Phe Val His Phe Leu Tyr Thr Met Val Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Cys Ala Arg Met Ala Leu Arg Ala Ser Gly Lys Tyr Ile Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Cys Ala Arg Lys Asn Gln Met Val Phe His Ala Arg Lys Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Cys Ala Arg Thr Gln Ser Phe Trp Glu Gln Gln Lys Val Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Cys	Ala	Arg	Tyr	Pro	Tyr	Arg	Ser	Asn	Phe	Phe	Met	Pro	Met	Asp	Val
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3..4

(D) OTHER INFORMATION: /product= "see Figure 10C"

/label= R*G

shift of /note= "* denotes codon with one-base deletion, causes
reading fr..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Cys	Ala	Arg	Gly	Ser	Gly	Ser	Glu	His	Trp	Ser	Ile	Phe	Asp	Val	Trp
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys Ala Arg Arg Asn Pro Trp Asn Val Asn Tyr Leu His Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Cys Ala Arg Met Lys Pro Met Leu Asn Arg Asp Gly Thr Met Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Cys Ala Arg Lys Gly Ser Glu Phe Leu Glu Thr Asp Val Met Asp Tyr
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

314

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Cys	Ala	Arg	Ser	Trp	Thr	Asn	Asp	Lys	Pro	Asn	Phe	Ile	Met	Asp	Val
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Cys	Ala	Arg	Tyr	Ala	Gly	Thr	Thr	Phe	Lys	Gln	Gly	Pro	Met	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Cys	Ala	Arg	Lys	Arg	Met	Met	Gln	Asn	Pro	Arg	Phe	Arg	Phe	Asp	Val
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:

315

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Cys Ala Arg Arg Ser Lys Gln Lys Arg Lys Met Arg Arg Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Cys Ala Arg Arg Asn Gly Lys Arg His Leu Arg His Arg Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Cys Ala Arg Arg Lys Met Arg Lys Arg Ile Lys Arg Arg Phe Asp Val
 1 5 10 15

316

Trp

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Cys	Ala	Arg	Tyr	Arg	Lys	Ile	Met	Lys	Trp	Lys	Asn	Ser	Phe	Asp	Val
1					5				10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Cys	Ala	Arg	Leu	Ile	Glu	Val	His	Pro	Ser	Phe	Asp	Gln	Met	Asp	Val
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

Cys Ala Arg Arg Lys Pro Met Phe Leu Lys Lys Ala Val Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Cys Ala Arg Arg Lys Phe His Arg Tyr Ser Thr Val Lys Phe Asp Tyr
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

Cys Ala Arg Arg Lys Thr Met Arg Ser Arg Val Lys Tyr Phe Asp Tyr
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid

318

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Cys	Ala	Arg	Lys	Lys	Arg	Ser	Trp	Arg	Arg	Met	Asp	Arg	Phe	Asp	Val
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

Cys	Ala	Arg	Arg	Asn	Pro	Arg	Arg	Gly	Arg	Met	Asn	Arg	Phe	Asp	Val
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Cys	Ala	Arg	Lys	Gly	Lys	Lys	Lys	Phe	Ala	Arg	Pro	Arg	Phe	Asp	Val
1				5					10					15	

Trp

319

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

Cys Ala Arg Arg Met Val His Lys Gly Lys Arg Lys Ile Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Cys Ala Arg Arg Lys His Ile Thr Tyr Pro Arg Lys Gln Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

Cys Ala Arg Arg Trp Thr Lys Arg Arg Ser Phe Ala Arg Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Cys Ala Arg Lys Lys Leu Lys Gln Tyr Thr Phe Ser Arg Phe Asp Tyr
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Cys Ala Arg Thr Arg Pro Trp Gln Ala Thr Arg Lys Gly Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Cys	Ala	Arg	Asn	Gln	Trp	Glu	Phe	Lys	Asn	Arg	Arg	Lys	Met	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Cys	Ala	Arg	Lys	Arg	Trp	Met	Trp	Pro	Ile	Gly	Lys	Arg	Phe	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

Cys	Ala	Arg	Tyr	Ser	Leu	Trp	Arg	Leu	Asp	Glu	Tyr	Phe	Phe	Asp	Tyr
1				5					10					15	

Trp

322

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Cys Ala Arg Val Pro Trp Gly Asp Phe Trp Ser Trp His Met Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Cys Ala Arg Asn Gly Leu Glu Pro Arg His Arg Lys Met Met Asp Tyr
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

323

Cys Ala Arg Ile Met Lys Ala Pro Pro Asp Tyr Trp
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Cys Ala Arg Arg Lys Thr Trp His Trp Phe Tyr Lys Arg Met Asp Tyr
 1 5 10 15
 Trp

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Cys Ala Arg Trp Lys Asp Met Trp Ser Gln Val Tyr Val Met Asp Tyr
 1 5 10 15
 Trp

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Cys Ala Arg Asn Lys Gln Gln Met Arg Phe Arg Arg Phe Met Asp Tyr
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Cys Ala Arg Asn Met Leu Ala Leu Ser Arg Gly Lys Glu Met Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Cys Ala Arg Asn Met Arg Leu Met Arg Met Arg Lys Asn Phe Asp Val
 1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid

325

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Cys	Ala	Arg	Tyr	Ile	Lys	Gln	Ala	Lys	Arg	Lys	Leu	Ala	Phe	Asp	Tyr
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Cys	Ala	Arg	Tyr	Asn	Arg	His	Ala	Trp	Gln	Lys	Met	Gln	Phe	Asp	Tyr
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Cys	Ala	Arg	Tyr	Val	Lys	Tyr	Ala	Arg	Asn	Lys	Met	Gln	Phe	Asp	Tyr
1				5				10						15	

Trp

326

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Cys	Ala	Arg	Tyr	Lys	Arg	Gly	Ala	Trp	Met	Lys	Thr	Met	Phe	Asp	Val
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Cys	Ala	Arg	Arg	Lys	Pro	Leu	Arg	Arg	Ile	Met	Lys	Trp	Phe	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Cys Ala Arg Tyr Arg Lys Arg Ala Ser Arg Gln Met Gln Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Cys Ala Arg Gln Arg Tyr Arg Ser Lys Ile Lys Gly His Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Cys Ala Arg Trp Arg Asp Phe Asn Ser Tyr Asp Pro Met Asp Tyr Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

328

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Cys	Ala	Arg	Met	Ala	Asp	Leu	Asp	Asn	Tyr	Trp	Val	Gln	Phe	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Cys	Ala	Arg	Leu	Gln	Ala	Tyr	Leu	Lys	Pro	His	His	Trp	Met	Asp	Tyr
1			5						10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Cys	Ala	Arg	Arg	Leu	Ile	Glu	Gln	Ala	Arg	Asp	His	Val	Met	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 242:

329

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Cys	Ala	Arg	Ser	Trp	His	Asn	Ser	Gln	Phe	Thr	Gln	Ser	Phe	Asp	Val
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Cys	Ala	Arg	Val	Asp	His	Phe	Gln	Thr	Glu	Asn	Glu	Trp	Met	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Cys Ala Arg Asp Trp Pro Thr Leu Ile Phe Trp Tyr Trp Phe Asp Tyr

330

Trp

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Cys Ala Arg Gly Phe Gly Phe Thr Glu Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Cys Ala Arg Gln Phe Asp Glu Asp Ser Phe Val Arg Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Cys Ala Arg Ile Leu Lys Glu Ser Ser Lys Ser Arg Gln Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Cys Ala Arg Glu Gln Asp Glu Tyr Gly Ala Ile Arg Ile Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Cys Ala Arg Asn His Phe Glu Ala Ser Trp Pro Arg Arg Gln Met Asp
1 5 10 15

Val Trp

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Cys Ala Arg Glu Asn Glu Trp Val Asp Met Ile Leu Asp Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Cys Ala Arg Gln Tyr Ser Glu Thr Arg Trp Val Arg Lys Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Cys Ala Arg Gln Phe Lys Glu Ser Lys Thr Arg Arg Lys Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Cys Ala Arg Lys Lys Thr Gln Tyr Val His Asp Trp Arg Met Asp Val
 1 5 10 15
 Trp

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Cys Ala Arg Arg Trp Arg Glu Thr Lys Ser Lys Arg Phe Phe Asp Val
 1 5 10 15
 Trp

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

334

Cys Ala Arg Asp Tyr Ile Met Glu Phe Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Cys Ala Arg Gln Phe Glu Glu Thr Lys Gln Arg Arg Leu Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Cys Ala Arg Asp Gln Gly Phe Tyr Ala Ile Asp Tyr Val Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Cys Ala Arg Val Phe Thr Tyr Met Tyr Asn Tyr Phe Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Cys Ala Arg Val Phe Phe Glu Gln Met Glu Val Val Arg Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Cys Ala Arg Glu Lys Glu Tyr Arg Leu Ser Trp Ser Gln Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid

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(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Cys Ala Arg Tyr Pro Ser Arg Trp Ala Pro Asn Trp Tyr Met Asp Tyr
1 5 10 15
Trp

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Cys Ala Arg Asp Gly Gly Phe Lys Pro Leu Thr His Phe Phe Asp Val
1 5 10 15
Trp

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "synthetic DNA cassette"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

ACATGTAAGC	TTCCCCCCCC	CCTTAATTAA	CCCCCCCCCC	TGTACACCCC	CCCCCGCTA	60
GGCCCCCCCC	CCAGATCTCC	CCCCCCCCCGA	CGTCCCCCCT	CTAGACCCCC	CCCCCGCATG	120
CCCCCCCCCC	CGAATTGAC	GTC				143

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(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 132..989
- (D) OTHER INFORMATION: /product= "Amp resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CAGGTGGCAC TTTTCGGGGA AATGTGCGCG GAACCCCTAT TTGTTTATTT TTCTAAATAC	60
ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCCTGATA AATGCTTCAA TAATATTGAA	120
AAAGGAAGAG T ATG AGT ATT CAA CAT TTC CGT GTC GCC CTT ATT CCC TTT	170
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe	
285 290	
TTT GCG GCA TTT TGC CTT CCT GTT TTT GCT CAC CCA GAA ACG CTG GTG	218
Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val	
295 300 305 310	
AAA GTA AAA GAT GCT GAA GAT CAG TTG GGT GCA CGA GTG GGT TAC ATC	266
Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile	
315 320 325	
GAA CTG GAT CTC AAC AGC GGT AAG ATC CTT GAG AGT TTT CGC CCC GAA	314
Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu	
330 335 340	
GAA CGT TTT CCA ATG ATG AGC ACT TTT AAA GTT CTG CTA TGT GGC GCG	362
Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala	
345 350 355	
GTA TTA TCC CGT ATT GAC GCC GGG CAA GAG CAA CTC GGT CGC CGC ATA	410
Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile	
360 365 370	
CAC TAT TCT CAG AAT GAC TTG GTT GAG TAC TCA CCA GTC ACA GAA AAG	458
His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys	
375 380 385 390	
CAT CTT ACG GAT GGC ATG ACA GTA AGA GAA TTA TGC AGT GCT GCC ATA	506
His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile	
395 400 405	
ACC ATG AGT GAT AAC ACT GCG GCC AAC TTA CTT CTG ACA ACG ATC GGA	554
Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly	
410 415 420	
GGA CCG AAG GAG CTA ACC GCT TTT TTG CAC AAC ATG GGG GAT CAT GTA	602

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Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	
		425					430					435				
ACT	CGC	CTT	GAT	CGT	TGG	GAA	CCG	GAG	CTG	AAT	GAA	GCC	ATA	CCA	AAC	650
Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	
	440					445					450					
GAC	GAG	CGT	GAC	ACC	ACG	ATG	CCT	GTA	GCA	ATG	GCA	ACA	ACG	TTG	CGC	698
Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	Val	Ala	Met	Ala	Thr	Thr	Leu	Arg	
455					460					465					470	
AAA	CTA	TTA	ACT	GGC	GAA	CTA	CTT	ACT	CTA	GCT	TCC	CGG	CAA	CAA	TTA	746
Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	
				475					480					485		
ATA	GAC	TGG	ATG	GAG	GCG	GAT	AAA	GTT	GCA	GGA	CCA	CTT	CTG	CGC	TCG	794
Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	
			490					495					500			
GCC	CTT	CCG	GCT	GGC	TGG	TTT	ATT	GCT	GAT	AAA	TCT	GGA	GCC	GGT	GAG	842
Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	
		505					510					515				
CGT	GGG	TCT	CGC	GGT	ATC	ATT	GCA	GCA	CTG	GGG	CCA	GAT	GGT	AAG	CCC	890
Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	
	520					525					530					
TCC	CGT	ATC	GTA	GTT	ATC	TAC	ACG	ACG	GGG	AGT	CAG	GCA	ACT	ATG	GAT	938
Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	
535					540					545					550	
GAA	CGA	AAT	AGA	CAG	ATC	GCT	GAG	ATA	GGT	GCC	TCA	CTG	ATT	AAG	CAT	986
Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	
				555					560					565		
TGG	TAACTGTCAG	ACCAAGTTTA	CTCATATATA	CTTTAGATTG	ATTTAAACT											1039
Trp																
TCATTTTAA	TTTAAAAGGA	TCTAGGTGAA	GATCCTTTTT	GATAATCTCA	TGACCAAAAT											1099
CCCTTAACGT	GAGTTTTTCGT	TCCACTGAGC	GTCAGACCCC	GTAGAAAAGA	TCAAAGGATC											1159
TTCTTGAGAT	CCTTTTTTTC	TGCGCGTAAT	CTGCTGCTTG	CAAACAAAAA	AACCACCGCT											1219
ACCAGCGGTG	GTTTGTTTTGC	CGGATCAAGA	GCTACCAACT	CTTTTTCCGA	AGGTAAGTGG											1279
CTTCAGCAGA	GCGCAGATAC	CAAATACTGT	CCTTCTAGTG	TAGCCGTAGT	TAGGCCACCA											1339
CTTCAAGAAC	TCTGTAGCAC	CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAAGTGGC											1399
TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	TCAAGACGAT	AGTTACCGGA											1459
TAAGGCGCAG	CGGTCGGGCT	GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC											1519
GACCTACACC	GAAGTACGAT	ACCTACAGCG	TGAGCTATGA	GAAAGCGCCA	CGCTTCCCGA											1579
AGGGAGAAAG	GCGGACAGGT	ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG											1639
GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	GTCGGGTTTC	GCCACCTCTG											1699
ACTTGAGCGT	CGATTTTTGT	GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG											1759



(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Met 1	Ser	Ile	Gln	His 5	Phe	Arg	Val	Ala	Leu 10	Ile	Pro	Phe	Phe	Ala	Ala 15
Phe	Cys	Leu	Pro 20	Val	Phe	Ala	His	Pro 25	Glu	Thr	Leu	Val	Lys 30	Val	Lys
Asp	Ala	Glu 35	Asp	Gln	Leu	Gly	Ala 40	Arg	Val	Gly	Tyr	Ile 45	Glu	Leu	Asp
Leu	Asn 50	Ser	Gly	Lys	Ile	Leu 55	Glu	Ser	Phe	Arg	Pro 60	Glu	Glu	Arg	Phe
Pro 65	Met	Met	Ser	Thr	Phe 70	Lys	Val	Leu	Leu	Cys 75	Gly	Ala	Val	Leu	Ser 80
Arg	Ile	Asp	Ala	Gly 85	Gln	Glu	Gln	Leu	Gly 90	Arg	Arg	Ile	His	Tyr 95	Ser
Gln	Asn	Asp	Leu 100	Val	Glu	Tyr	Ser	Pro 105	Val	Thr	Glu	Lys	His 110	Leu	Thr
Asp	Gly	Met 115	Thr	Val	Arg	Glu	Leu 120	Cys	Ser	Ala	Ala	Ile 125	Thr	Met	Ser
Asp	Asn 130	Thr	Ala	Ala	Asn	Leu 135	Leu	Leu	Thr	Thr	Ile 140	Gly	Gly	Pro	Lys
Glu 145	Leu	Thr	Ala	Phe 150	Leu	His	Asn	Met	Gly	Asp 155	His	Val	Thr	Arg	Leu 160
Asp	Arg	Trp	Glu	Pro 165	Glu	Leu	Asn	Glu	Ala 170	Ile	Pro	Asn	Asp	Glu 175	Arg
Asp	Thr	Thr	Met 180	Pro	Val	Ala	Met	Ala 185	Thr	Thr	Leu	Arg	Lys 190	Leu	Leu
Thr	Gly	Glu 195	Leu	Leu	Thr	Leu	Ala 200	Ser	Arg	Gln	Gln	Leu 205	Ile	Asp	Trp
Met 210	Glu	Ala	Asp	Lys	Val	Ala 215	Gly	Pro	Leu	Leu	Arg 220	Ser	Ala	Leu	Pro

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Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
 275 280 285

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GACGTCTTAA TGTGAGTTAG CTCCTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC 60
 CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG 120
 ACCATGATTA CGAATTTCTA GA 142

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: /product= "gIIIp ss with myc-tag, amber codon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

GAA TTC GAG CAG AAG CTG ATC TCT GAG GAG GAT CTG TAG GGT GGT GGC 48
 Glu Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu * Gly Gly Gly
 290 295 300
 TCT GGT TCC GGT GAT TTT GAT TAT GAA AAG ATG GCA AAC GCT AAT AAG 96
 Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys
 305 310 315

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GGG GCT ATG ACC GAA AAT GCC GAT GAA AAC GCG CTA CAG TCT GAC GCT Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala 320 325 330	144
AAA GGC AAA CTT GAT TCT GTC GCT ACT GAT TAC GGT GCT GCT ATC GAT Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp 335 340 345 350	192
GGT TTC ATT GGT GAC GTT TCC GGC CTT GCT AAT GGT AAT GGT GCT ACT Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr 355 360 365	240
GGT GAT TTT GCT GGC TCT AAT TCC CAA ATG GCT CAA GTC GGT GAC GGT Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly 370 375 380	288
GAT AAT TCA CCT TTA ATG AAT AAT TTC CGT CAA TAT TTA CCT TCC CTC Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu 385 390 395	336
CCT CAA TCG GTT GAA TGT CGC CCT TTT GTC TTT GGC GCT GGT AAA CCA Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro 400 405 410	384
TAT GAA TTT TCT ATT GAT TGT GAC AAA ATA AAC TTA TTC CGT GGT GTC Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val 415 420 425 430	432
TTT GCG TTT CTT TTA TAT GTT GCC ACC TTT ATG TAT GTA TTT TCT ACG Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr 435 440 445	480
TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT TGATAAGCTT Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser 450 455	520

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Glu Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu * Gly Gly Gly 1 5 10 15
Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys 20 25 30
Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala 35 40 45
Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp 50 55 60
Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr 65 70 75 80

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Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly
 85 90 95

Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu
 100 105 110

Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro
 115 120 125

Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val
 130 135 140

Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr
 145 150 155 160

Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 165 170

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GGGGGGGGGG AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG ACATTTTTTTT 60

TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG GGGGGGGTGT ACAGGGGGGG 120

GGG 123

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

GCTAGCACGC GCCCTGTAGC GGCGCATTA GCGCGGCGGG TGTGGTGGTT ACGCGCAGCG 60

TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT CGCTTTCCTT CCTTCCTTTC 120

TCGCCACGTT CGCCGGCTTT CCCCCTCAAG CTCTAAATCG GGGCATCCCT TTAGGGTTCC 180

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GATTTAGTGC TTTACGGCAC CTCGACCCCA AAAAAGTTGA TTAGGGTGAT GGTTCCTCGTA	240
GTGGGCCATC GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA	300
ATAGTGGACT CTGTGTTCAA ACTGGAACAA CACTCAACCC TATCTCGGTC TATTCTTTTG	360
ATTTATAAGG GATTTTGCCG ATTTCCGCCT ATTGGTTAAA AAATGAGCTG ATTTAACAAA	420
AAATTAACGC GAATTTTAAC AAAATATTAA CGTTTACAAT TTCATGTACA	470

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGATCTGACC AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTTAGA	60
AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC	120
AAAAAAACCA CCGCTACCAG CCGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT	180
TCCGAAGGTA ACTGGCTACA GCAGAGCGCA GATACCAAAT ACTGTTCTTC TAGTGTAGCC	240
GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT	300
CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG	360
ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC	420
CAGCTTGAG CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG	480
CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC	540
AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCTG	600
GTTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GGCGGAGCCT	660
ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCTCTG GCCTTTTGCT GGCCTTTTGC	720
TCACATGGCT AGC	733

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:102..758

(D) OTHER INFORMATION:/product= "cat resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

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GGGACGTCGG GTGAGGTTCC AACTTTCACC ATAATGAAAT AAGATCACTA CCGGGCGTAT      60
TTTTTGAGTT ATCGAGATTT TCAGGAGCTA AGGAAGCTAA A ATG GAG AAA AAA      113
                               Met Glu Lys Lys

ATC ACT GGA TAT ACC ACC GTT GAT ATA TCC CAA TGG CAT CGT AAA GAA      161
Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp His Arg Lys Glu
175                               180                               185                               190

CAT TTT GAG GCA TTT CAG TCA GTT GCT CAA TGT ACC TAT AAC CAG ACC      209
His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr Tyr Asn Gln Thr
                               195                               200                               205

GTT CAG CTG GAT ATT ACG GCC TTT TTA AAG ACC GTA AAG AAA AAT AAG      257
Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val Lys Lys Asn Lys
                               210                               215                               220

CAC AAG TTT TAT CCG GCC TTT ATT CAC ATT CTT GCC CGC CTG ATG AAT      305
His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala Arg Leu Met Asn
                               225                               230                               235

GCT CAC CCG GAG TTC CGT ATG GCA ATG AAA GAC GGT GAG CTG GTG ATA      353
Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly Glu Leu Val Ile
                               240                               245                               250

TGG GAT AGT GTT CAC CCT TGT TAC ACC GTT TTC CAT GAG CAA ACT GAA      401
Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His Glu Gln Thr Glu
255                               260                               265                               270

ACG TTT TCA TCG CTC TGG AGT GAA TAC CAC GAC GAT TTC CGG CAG TTT      449
Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp Phe Arg Gln Phe
                               275                               280                               285

CTA CAC ATA TAT TCG CAA GAT GTG GCG TGT TAC GGT GAA AAC CTG GCC      497
Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly Glu Asn Leu Ala
                               290                               295                               300

TAT TTC CCT AAA GGG TTT ATT GAG AAT ATG TTT TTC GTC TCA GCC AAT      545
Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe Val Ser Ala Asn
                               305                               310                               315

CCC TGG GTG AGT TTC ACC AGT TTT GAT TTA AAC GTA GCC AAT ATG GAC      593
Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val Ala Asn Met Asp
                               320                               325                               330

AAC TTC TTC GCC CCC GTT TTC ACT ATG GGC AAA TAT TAT ACG CAA GGC      641
Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr Tyr Thr Gln Gly
335                               340                               345                               350

GAC AAG GTG CTG ATG CCG CTG GCG ATT CAG GTT CAT CAT GCC GTT TGT      689

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Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His His Ala Val Cys
 355 360 365

GAT GGC TTC CAT GTC GGC AGA ATG CTT AAT GAA TTA CAA CAG TAC TGC 737
 Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu Gln Gln Tyr Cys
 370 375 380

GAT GAG TGG CAG GGC GGG GCG TAATTTTTTTT AAGGCAGTTA TTGGGTGCCC 788
 Asp Glu Trp Gln Gly Gly Ala
 385

TTAAACGCCT GGTGCTAGAT CTTCC 813

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp
 1 5 10 15

His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
 20 25 30

Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
 35 40 45

Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
 50 55 60

Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly
 65 70 75 80

Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His
 85 90 95

Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp
 100 105 110

Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly
 115 120 125

Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe
 130 135 140

Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
 145 150 155 160

Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
 165 170 175

Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
 180 185 190

His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
 195 200 205

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Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
210 215

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509
- (D) OTHER INFORMATION: /product= "gIIIp ss, myc tag, amber codon"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (1853..2509)
- (D) OTHER INFORMATION: /product= "cat resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

AA TTC GAG CAG AAG CTG ATC TCT GAG GAG GAT CTG TAG GGT GGT GGC Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu * Gly Gly Gly 220 225 230	47
TCT GGT TCC GGT GAT TTT GAT TAT GAA AAG ATG GCA AAC GCT AAT AAG Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys 235 240 245 250	95
GGG GCT ATG ACC GAA AAT GCC GAT GAA AAC GCG CTA CAG TCT GAC GCT Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala 255 260 265	143
AAA GGC AAA CTT GAT TCT GTC GCT ACT GAT TAC GGT GCT GCT ATC GAT Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp 270 275 280	191
GGT TTC ATT GGT GAC GTT TCC GGC CTT GCT AAT GGT AAT GGT GCT ACT Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr 285 290 295	239
GGT GAT TTT GCT GGC TCT AAT TCC CAA ATG GCT CAA GTC GGT GAC GGT Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly 300 305 310	287
GAT AAT TCA CCT TTA ATG AAT AAT TTC CGT CAA TAT TTA CCT TCC CTC Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu 315 320 325 330	335
CCT CAA TCG GTT GAA TGT CGC CCT TTT GTC TTT GGC GCT GGT AAA CCA Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro 335 340 345	383

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TAT GAA TTT TCT ATT GAT TGT GAC AAA ATA AAC TTA TTC CGT GGT GTC Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val 350 355 360	431
TTT GCG TTT CTT TTA TAT GTT GCC ACC TTT ATG TAT GTA TTT TCT ACG Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr 365 370 375	479
TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT TGATAAGCTT GACCTGTGAA Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser 380 385	529
GTGAAAAATG GCGCAGATTG TGCACATTT TTTTGTCTG CCGTTTAATT AAAGGGGGGG	589
GGGGGCCGGC CTGGGGGGGG GTGTACATGA AATTGTAAAC GTTAATATTT TGTTAAAATT	649
CGCGTTAAAT TTTTGTAAAT TCAGTCTATT TTTTAACCAA TAGGCCGAAA TCGGCAAAAT	709
CCCTTATAAA TCAAAAGAAT AGACCGAGAT AGGGTTGAGT GTTGTTCCAG TTTGGAACAA	769
GAGTCCACTA TTAAAGAACG TGGACTCCAA CGTCAAAGGG CGAAAAACCG TCTATCAGGG	829
CGATGGCCCA CTACGAGAAC CATCACCTTA ATCAAGTTTT TTGGGGTCGA GGTGCCGTAA	889
AGCACTAAAT CGGAACCTTA AAGGGAGCCC CCGATTTAGA GCTTGACGGG GAAAGCCGGC	949
GAACGTGGCG AGAAAGGAAG GGAAGAAAGC GAAAGGAGCG GGCGCTAGGG CGCTGGCAAG	1009
TGTAGCGGTC ACGCTGCGCG TAACCACCAC ACCCGCCGCG CTTAATGCGC CGCTACAGGG	1069
CGCGTGCTAG CCATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG	1129
TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAACAAA TCGACGCTCA	1189
AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC	1249
TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC CGCCTTTCTC	1309
CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA GGTATCTCAG TTCGGTGTAG	1369
GTCGTTGCTT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA CCGCTGCGCC	1429
TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA	1489
GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG	1549
AAGTGGTGGC CTAACCTACGG CTACACTAGA AGAACAGTAT TTGGTATCTG CGCTCTGCTG	1609
TAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT	1669
GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA	1729
GAAGATCCTT TGATCTTTTC TACGGGTCTT GACGCTCAGT GGAACGAAAA CTCACGTAA	1789
GGGATTTTGG TCAGATCTAG CACCAGGCGT TTAAGGGCAC CAATAACTGC CTTAAAAAAA	1849
TTACGCCCCG CCCTGCCACT CATCGCAGTA CTGTTGTAAT TCATTAAGCA TTCTGCCGAC	1909
ATGGAAGCCA TCACAAACGG CATGATGAAC CTGAATCGCC AGCGGCATCA GCACCTTGTC	1969
GCCTTGCGTA TAATATTTGC CCATAGTGAA AACGGGGGCG AAGAAGTTGT CCATATTGGC	2029

TACGTTTAAA TCAAACTGG TGAACTCAC CCAGGGATTG GCTGAGACGA AAAACATATT 2089
 CTCAATAAAC CCTTTAGGGA AATAGGCCAG GTTTTCACCG TAACACGCCA CATCTTGCGA 2149
 ATATATGTGT AGAACTGCC GGAAATCGTC GTGGTATTCA CTCCAGAGCG ATGAAAACGT 2209
 TTCAGTTTGC TCATGGAAAA CGGTGTAACA AGGGTGAACA CTATCCCATA TCACCAGCTC 2269
 ACCGTCTTTC ATTGCCATAC GGAAGTCCGG GTGAGCATTC ATCAGGCGGG CAAGAATGTG 2329
 AATAAAGGCC GGATAAACT TGTGCTTATT TTTCTTTACG GTCTTTAAAA AGGCCGTAAT 2389
 ATCCAGCTGA ACGGTCTGGT TATAGGTACA TTGAGCAACT GACTGAAATG CCTCAAAATG 2449
 TTCTTTACGA TGCCATTGGG ATATATCAAC GGTGGTATAT CCAGTGATTT TTTTCTCCAT 2509
 TTTAGCTTCC TTAGCTCCTG AAAATCTCGA TAACTCAAAA AATACGCCCG GTAGTGATCT 2569
 TATTTTCATTA TGGTGAAAGT TGAACCTCA CCGACGTCT AATGTGAGTT AGCTCACTCA 2629
 TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG 2689
 CGGATAACAA TTTACACAG GAAACAGCTA TGACCATGAT TACGAATTC TAGAGCATGC 2749
 GGGGGG 2755

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu * Gly Gly Gly Ser
 1 5 10 15
 Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly
 20 25 30
 Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys
 35 40 45
 Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly
 50 55 60
 Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly
 65 70 75 80
 Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp
 85 90 95
 Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro
 100 105 110
 Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro Tyr
 115 120 125
 Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe

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130		135		140
Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe				
145		150		155 160
Ala Asn Ile Leu Arg Asn Lys Glu Ser				
		165		

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Met	Glu	Lys	Lys	Ile	Thr	Gly	Tyr	Thr	Thr	Val	Asp	Ile	Ser	Gln	Trp	1	5	10	15
His	Arg	Lys	Glu	His	Phe	Glu	Ala	Phe	Gln	Ser	Val	Ala	Gln	Cys	Thr	20	25	30	
Tyr	Asn	Gln	Thr	Val	Gln	Leu	Asp	Ile	Thr	Ala	Phe	Leu	Lys	Thr	Val	35	40	45	
Lys	Lys	Asn	Lys	His	Lys	Phe	Tyr	Pro	Ala	Phe	Ile	His	Ile	Leu	Ala	50	55	60	
Arg	Leu	Met	Asn	Ala	His	Pro	Glu	Phe	Arg	Met	Ala	Met	Lys	Asp	Gly	65	70	75	80
Glu	Leu	Val	Ile	Trp	Asp	Ser	Val	His	Pro	Cys	Tyr	Thr	Val	Phe	His	85	90	95	
Glu	Gln	Thr	Glu	Thr	Phe	Ser	Ser	Leu	Trp	Ser	Glu	Tyr	His	Asp	Asp	100	105	110	
Phe	Arg	Gln	Phe	Leu	His	Ile	Tyr	Ser	Gln	Asp	Val	Ala	Cys	Tyr	Gly	115	120	125	
Glu	Asn	Leu	Ala	Tyr	Phe	Pro	Lys	Gly	Phe	Ile	Glu	Asn	Met	Phe	Phe	130	135	140	
Val	Ser	Ala	Asn	Pro	Trp	Val	Ser	Phe	Thr	Ser	Phe	Asp	Leu	Asn	Val	145	150	155	160
Ala	Asn	Met	Asp	Asn	Phe	Phe	Ala	Pro	Val	Phe	Thr	Met	Gly	Lys	Tyr	165	170	175	
Tyr	Thr	Gln	Gly	Asp	Lys	Val	Leu	Met	Pro	Leu	Ala	Ile	Gln	Val	His	180	185	190	
His	Ala	Val	Cys	Asp	Gly	Phe	His	Val	Gly	Arg	Met	Leu	Asn	Glu	Leu	195	200	205	
Gln	Gln	Tyr	Cys	Asp	Glu	Trp	Gln	Gly	Gly	Ala						210	215		

(2) INFORMATION FOR SEQ ID NO: 277:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```

GACGTCCTTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC      60
CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG      120
ACCATGTCTA GAATAACTTC GTATAATGTA CGCTATACGA AGTTATCGCA TGC              173

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(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

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AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TGACGTC                      47

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(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1245
- (D) OTHER INFORMATION: /product= "gIIIp, GGGGS linker"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

GAA TTC GGT GGT GGT GGA TCT GCG TGC GCT GAA ACG GTT GAA AGT TGT      48
Glu Phe Gly Gly Gly Gly Ser Ala Cys Ala Glu Thr Val Glu Ser Cys
220                225                230                235

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TTA	GCA	AAA	TCC	CAT	ACA	GAA	AAT	TCA	TTT	ACT	AAC	GTC	TGG	AAA	GAC	96
Leu	Ala	Lys	Ser	His	Thr	Glu	Asn	Ser	Phe	Thr	Asn	Val	Trp	Lys	Asp	
				240					245					250		
GAC	AAA	ACT	TTA	GAT	CGT	TAC	GCT	AAC	TAT	GAG	GGC	TGT	CTG	TGG	AAT	144
Asp	Lys	Thr	Leu	Asp	Arg	Tyr	Ala	Asn	Tyr	Glu	Gly	Cys	Leu	Trp	Asn	
			255					260					265			
GCT	ACA	GGC	GTT	GTA	GTT	TGT	ACT	GGT	GAC	GAA	ACT	CAG	TGT	TAC	GGT	192
Ala	Thr	Gly	Val	Val	Val	Cys	Thr	Gly	Asp	Glu	Thr	Gln	Cys	Tyr	Gly	
		270					275					280				
ACA	TGG	GTT	CCT	ATT	GGG	CTT	GCT	ATC	CCT	GAA	AAT	GAG	GGT	GGT	GGC	240
Thr	Trp	Val	Pro	Ile	Gly	Leu	Ala	Ile	Pro	Glu	Asn	Glu	Gly	Gly	Gly	
	285					290					295					
TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGT	ACT	288
Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Thr	
300					305					310					315	
AAA	CCT	CCT	GAG	TAC	GGT	GAT	ACA	CCT	ATT	CCG	GGC	TAT	ACT	TAT	ATC	336
Lys	Pro	Pro	Glu	Tyr	Gly	Asp	Thr	Pro	Ile	Pro	Gly	Tyr	Thr	Tyr	Ile	
				320					325					330		
AAC	CCT	CTC	GAC	GGC	ACT	TAT	CCG	CCT	GGT	ACT	GAG	CAA	AAC	CCC	GCT	384
Asn	Pro	Leu	Asp	Gly	Thr	Tyr	Pro	Pro	Gly	Thr	Glu	Gln	Asn	Pro	Ala	
			335					340					345			
AAT	CCT	AAT	CCT	TCT	CTT	GAG	GAG	TCT	CAG	CCT	CTT	AAT	ACT	TTC	ATG	432
Asn	Pro	Asn	Pro	Ser	Leu	Glu	Glu	Ser	Gln	Pro	Leu	Asn	Thr	Phe	Met	
		350					355					360				
TTT	CAG	AAT	AAT	AGG	TTC	CGA	AAT	AGG	CAG	GGG	GCA	TTA	ACT	GTT	TAT	480
Phe	Gln	Asn	Asn	Arg	Phe	Arg	Asn	Arg	Gln	Gly	Ala	Leu	Thr	Val	Tyr	
	365					370					375					
ACG	GGC	ACT	GTT	ACT	CAA	GGC	ACT	GAC	CCC	GTT	AAA	ACT	TAT	TAC	CAG	528
Thr	Gly	Thr	Val	Thr	Gln	Gly	Thr	Asp	Pro	Val	Lys	Thr	Tyr	Tyr	Gln	
380					385					390					395	
TAC	ACT	CCT	GTA	TCA	TCA	AAA	GCC	ATG	TAT	GAC	GCT	TAC	TGG	AAC	GGT	576
Tyr	Thr	Pro	Val	Ser	Ser	Lys	Ala	Met	Tyr	Asp	Ala	Tyr	Trp	Asn	Gly	
				400				405					410			
AAA	TTC	AGA	GAC	TGC	GCT	TTC	CAT	TCT	GGC	TTT	AAT	GAG	GAT	TTA	TTT	624
Lys	Phe	Arg	Asp	Cys	Ala	Phe	His	Ser	Gly	Phe	Asn	Glu	Asp	Leu	Phe	
			415					420				425				
GTT	TGT	GAA	TAT	CAA	GGC	CAA	TCG	TCT	GAC	CTG	CCT	CAA	CCT	CCT	GTC	672
Val	Cys	Glu	Tyr	Gln	Gly	Gln	Ser	Ser	Asp	Leu	Pro	Gln	Pro	Pro	Val	
		430					435					440				
AAT	GCT	GGC	GGC	GGC	TCT	GGT	GGT	GGT	TCT	GGT	GGC	GGC	TCT	GAG	GGT	720
Asn	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Gly	
		445				450					455					
GGT	GGC	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGC	TCT	GAG	GGA	GGC	768
Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	
460					465				470						475	
GGT	TCC	GGT	GGT	GGC	TCT	GGT	TCC	GGT	GAT	TTT	GAT	TAT	GAA	AAG	ATG	816

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Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Lys	Met	
				480					485					490		
GCA	AAC	GCT	AAT	AAG	GGG	GCT	ATG	ACC	GAA	AAT	GCC	GAT	GAA	AAC	GCG	864
Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	Asn	Ala	Asp	Glu	Asn	Ala	
			495					500					505			
CTA	CAG	TCT	GAC	GCT	AAA	GGC	AAA	CTT	GAT	TCT	GTC	GCT	ACT	GAT	TAC	912
Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	Asp	Ser	Val	Ala	Thr	Asp	Tyr	
		510					515					520				
GGT	GCT	GCT	ATC	GAT	GGT	TTC	ATT	GGT	GAC	GTT	TCC	GGC	CTT	GCT	AAT	960
Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	Gly	Asp	Val	Ser	Gly	Leu	Ala	Asn	
	525					530					535					
GGT	AAT	GGT	GCT	ACT	GGT	GAT	TTT	GCT	GGC	TCT	AAT	TCC	CAA	ATG	GCT	1008
Gly	Asn	Gly	Ala	Thr	Gly	Asp	Phe	Ala	Gly	Ser	Asn	Ser	Gln	Met	Ala	
	540				545					550				555		
CAA	GTC	GGT	GAA	GGT	GAT	AAT	TCA	CCT	TTA	ATG	AAT	AAT	TTC	CGT	CAA	1056
Gln	Val	Gly	Glu	Gly	Asp	Asn	Ser	Pro	Leu	Met	Asn	Asn	Phe	Arg	Gln	
				560					565					570		
TAT	TTA	CCT	TCC	ATC	CCT	CAA	TCG	GTT	GAA	TGT	CGC	CCT	TTT	GTC	TTT	1104
Tyr	Leu	Pro	Ser	Ile	Pro	Gln	Ser	Val	Glu	Cys	Arg	Pro	Phe	Val	Phe	
			575					580					585			
GGC	GCT	GGT	AAA	CCC	TAT	GAA	TTT	TCT	ATT	GAT	TGT	GAC	AAA	ATA	AAC	1152
Gly	Ala	Gly	Lys	Pro	Tyr	Glu	Phe	Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	
		590					595					600				
TTA	TTC	CGT	GGT	GTC	TTT	GCG	TTT	CTT	TTA	TAT	GTT	GCC	ACC	TTT	ATG	1200
Leu	Phe	Arg	Gly	Val	Phe	Ala	Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	
	605					610					615					
TAT	GTA	TTT	TCT	ACG	TTT	GCT	AAC	ATA	CTG	CGT	AAT	AAG	GAG	TCT		1245
Tyr	Val	Phe	Ser	Thr	Phe	Ala	Asn	Ile	Leu	Arg	Asn	Lys	Glu	Ser		
	620				625					630						
TGATAAGCTT																1255

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Glu Phe Gly Gly Gly Gly Ser Ala Cys Ala Glu Thr Val Glu Ser Cys
 1 5 10 15
 Leu Ala Lys Ser His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys Asp
 20 25 30
 Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn
 35 40 45
 Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly

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50					55					60					
Thr 65	Trp	Val	Pro	Ile	Gly 70	Leu	Ala	Ile	Pro	Glu 75	Asn	Glu	Gly	Gly	Gly 80
Ser	Glu	Gly	Gly	Gly 85	Ser	Glu	Gly	Gly	Gly 90	Ser	Glu	Gly	Gly	Gly 95	Thr
Lys	Pro	Pro	Glu 100	Tyr	Gly	Asp	Thr	Pro	Ile 105	Pro	Gly	Tyr	Thr	Tyr 110	Ile
Asn	Pro	Leu 115	Asp	Gly	Thr	Tyr	Pro	Pro	Gly 120	Thr	Glu	Gln	Asn	Pro	Ala
Asn	Pro 130	Asn	Pro	Ser	Leu	Glu 135	Glu	Ser	Gln	Pro	Leu 140	Asn	Thr	Phe	Met
Phe 145	Gln	Asn	Asn	Arg	Phe 150	Arg	Asn	Arg	Gln	Gly 155	Ala	Leu	Thr	Val	Tyr 160
Thr	Gly	Thr	Val	Thr 165	Gln	Gly	Thr	Asp	Pro 170	Val	Lys	Thr	Tyr	Tyr 175	Gln
Tyr	Thr	Pro	Val 180	Ser	Ser	Lys	Ala	Met	Tyr 185	Asp	Ala	Tyr	Trp	Asn 190	Gly
Lys	Phe	Arg 195	Asp	Cys	Ala	Phe	His 200	Ser	Gly	Phe	Asn	Glu 205	Asp	Leu	Phe
Val	Cys 210	Glu	Tyr	Gln	Gly	Gln 215	Ser	Ser	Asp	Leu	Pro 220	Gln	Pro	Pro	Val
Asn 225	Ala	Gly	Gly	Gly	Ser 230	Gly	Gly	Gly	Ser	Gly 235	Gly	Gly	Ser	Glu	Gly 240
Gly	Gly	Ser	Glu	Gly 245	Gly	Gly	Ser	Glu	Gly 250	Gly	Gly	Ser	Glu	Gly 255	Gly
Gly	Ser	Gly 260	Gly	Gly	Ser	Gly	Ser	Gly 265	Asp	Phe	Asp	Tyr	Glu 270	Lys	Met
Ala	Asn	Ala 275	Asn	Lys	Gly	Ala	Met 280	Thr	Glu	Asn	Ala	Asp 285	Glu	Asn	Ala
Leu 290	Gln	Ser	Asp	Ala	Lys	Gly 295	Lys	Leu	Asp	Ser	Val 300	Ala	Thr	Asp	Tyr
Gly 305	Ala	Ala	Ile	Asp	Gly 310	Phe	Ile	Gly	Asp	Val 315	Ser	Gly	Leu	Ala	Asn 320
Gly	Asn	Gly	Ala 325	Thr	Gly	Asp	Phe	Ala	Gly 330	Ser	Asn	Ser	Gln	Met 335	Ala
Gln	Val	Gly	Glu 340	Gly	Asp	Asn	Ser	Pro 345	Leu	Met	Asn	Asn	Phe	Arg 350	Gln
Tyr	Leu 355	Pro	Ser	Ile	Pro	Gln	Ser	Val 360	Glu	Cys	Arg	Pro	Phe	Val 365	Phe
Gly 370	Ala	Gly	Lys	Pro	Tyr	Glu 375	Phe	Ser	Ile	Asp	Cys 380	Asp	Lys	Ile	Asn

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Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met
385 390 395 400

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
405 410 415

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..492
- (D) OTHER INFORMATION: /product= "gIIIp ss"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

CGG GAA TTC GGA GGC GGT TCC GGT GGT GGC TCT GGT TCC GGT GAT TTT	48
Glu Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe	
420 425 430	
GAT TAT GAA AAG ATG GCA AAC GCT AAT AAG GGG GCT ATG ACC GAA AAT	96
Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn	
435 440 445	
GCC GAT GAA AAC GCG CTA CAG TCT GAC GCT AAA GGC AAA CTT GAT TCT	144
Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser	
450 455 460	
GTC GCT ACT GAT TAC GGT GCT GCT ATC GAT GGT TTC ATT GGT GAC GTT	192
Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val	
465 470 475	
TCC GGC CTT GCT AAT GGT AAT GGT GCT ACT GGT GAT TTT GCT GGC TCT	240
Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser	
480 485 490	
AAT TCC CAA ATG GCT CAA GTC GGT GAC GGT GAT AAT TCA CCT TTA ATG	288
Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met	
495 500 505 510	
AAT AAT TTC CGT CAA TAT TTA CCT TCC CTC CCT CAA TCG GTT GAA TGT	336
Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys	
515 520 525	
CGC CCT TTT GTC TTT GGC GCT GGT AAA CCA TAT GAA TTT TCT ATT GAT	384
Arg Pro Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp	
530 535 540	
TGT GAC AAA ATA AAC TTA TTC CGT GGT GTC TTT GCG TTT CTT TTA TAT	432
Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr	
545 550 555	

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GTT GCC ACC TTT ATG TAT GTA TTT TCT ACG TTT GCT AAC ATA CTG CGT 480
 Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg
 560 565 570

AAT AAG GAG TCT TGATAAGCTT 502
 Asn Lys Glu Ser
 575

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

Glu Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp
 1 5 10 15
 Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala
 20 25 30
 Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val
 35 40 45
 Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser
 50 55 60
 Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn
 65 70 75 80
 Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn
 85 90 95
 Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg
 100 105 110
 Pro Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys
 115 120 125
 Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val
 130 135 140
 Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn
 145 150 155 160
 Lys Glu Ser

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GCATGCCATA ACTTCGTATA ATGTACGCTA TACGAAGTTA TAAGCTT

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(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 82..978
- (D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

GGGGGTGTAC ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCTGATA AATGCTTCAA	60
TAATATTGAA AAAGGAAGAG T ATG AGT ATT CAA CAT TTC CGT GTC GCC CTT	111
Met Ser Ile Gln His Phe Arg Val Ala Leu	
165 170	
ATT CCC TTT TTT GCG GCA TTT TGC CTT CCT GTT TTT GCT CAC CCA GAA	159
Ile Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu	
175 180 185	
ACG CTG GTG AAA GTA AAA GAT GCT GAG GAT CAG TTG GGT GCG CGA GTG	207
Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val	
190 195 200 205	
GGT TAC ATC GAA CTG GAT CTC AAC AGC GGT AAG ATC CTT GAG AGT TTT	255
Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe	
210 215 220	
CGC CCC GAA GAA CGT TTT CCA ATG ATG AGC ACT TTT AAA GTT CTG CTA	303
Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu	
225 230 235	
TGT GGC GCG GTA TTA TCC CGT ATT GAC GCC GGG CAA GAG CAA CTC GGT	351
Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly	
240 245 250	
CGC CGC ATA CAC TAT TCT CAG AAT GAC TTG GTT GAG TAC TCA CCA GTC	399
Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val	
255 260 265	
ACA GAA AAG CAT CTT ACG GAT GGC ATG ACA GTA AGA GAA TTA TGC AGT	447
Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser	
270 275 280 285	

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GCT GCC ATA ACC ATG AGT GAT AAC ACT GCG GCC AAC TTA CTT CTG ACA	495
Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr	
290 295 300	
ACG ATC GGA GGA CCG AAG GAG CTA ACC GCT TTT TTG CAC AAC ATG GGG	543
Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly	
305 310 315	
GAT CAT GTA ACT CGC CTT GAT CGT TGG GAA CCG GAG CTG AAT GAA GCC	591
Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala	
320 325 330	
ATA CCA AAC GAC GAG CGT GAC ACC ACG ATG CCT GTA GCA ATG GCA ACA	639
Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala Met Ala Thr	
335 340 345	
ACG TTG CGC AAA CTA TTA ACT GGC GAA CTA CTT ACT CTA GCT TCC CGG	687
Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg	
350 355 360 365	
CAA CAG TTA ATA GAC TGG ATG GAG GCG GAT AAA GTT GCA GGA CCA CTT	735
Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu	
370 375 380	
CTG CGC TCG GCC CTT CCG GCT GGC TGG TTT ATT GCT GAT AAA TCT GGA	783
Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly	
385 390 395	
GCC GGT GAG CGT GGG TCT CGC GGT ATC ATT GCA GCA CTG GGG CCA GAT	831
Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp	
400 405 410	
GGT AAG CCC TCC CGT ATC GTA GTT ATC TAC ACG ACG GGG AGT CAG GCA	879
Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala	
415 420 425	
ACT ATG GAT GAA CGA AAT AGA CAG ATC GCT GAG ATA GGT GCC TCA CTG	927
Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu	
430 435 440 445	
ATT AAG CAT TGG GTA ACT GTC AGA CCA AGT TTA CTC ATA TAT ACT TTA	975
Ile Lys His Trp Val Thr Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu	
450 455 460	
GAT TGATTTAAAA CTTCAATTTTT AATTTAAAAG GATCTAGGTG AAGATCCTTT	1028
Asp	
TTGATAATCT CATGACCAAA ATCCCTTAAC GTGAGTTTTT GTTCCACTGA GCGTCAGACC	1088
CCGTAGAAAA GATCAAAGGA TCTTCTTGAG ATCCTTTTTT ATAATGGCCG GCGGGGGGGG	1148
TTAATTAAGG GGGGG	1163

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

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Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1              5              10              15
Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
              20              25              30
Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
              35              40              45
Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
              50              55              60
Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
              65              70              75              80
Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
              85              90              95
Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
              100              105              110
Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
              115              120              125
Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
              130              135              140
Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
              145              150              155              160
Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
              165              170              175
Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
              180              185              190
Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
              195              200              205
Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
              210              215              220
Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
              225              230              235              240
Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
              245              250              255
Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
              260              265              270
Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Val Thr
              275              280              285
Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu Asp
              290              295

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(2) INFORMATION FOR SEQ ID NO: 286:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

GCTAGCACGC GCCCTGTAGC GGCGCATTA	60
GGCGCGCGGG TGTGGTGGTT ACGCGCAGCG	
TGACCGCTAC ACTTGCCAGC GCCCTAGCGC	120
CCGCTCCTTT CGCTTTCCTTC CCTTCCTTTC	
TCGCCACGTT CGCCGGCTTT CCCCCTCAAG	180
CTCTAAATCG GGGGCTCCCT TTAGGGTTCC	
GATTTAGTGC TTTACGGCAC CTCGACCCCA	240
AAAAACTTGA TTAGGGTGAT GGTTCTCGTA	
GTGGGCCATC GCCCTGATAG ACGGTTTTTC	300
GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA	
ATAGTGGACT CTTGTTCCAA ACTGGAACAA	360
CACTCAACCC TATCTCGGTC TATTCTTTTG	
ATTTATAAGG GATTTTGCCG ATTTCGGCCT	420
ATTGGTTAAA AAATGAGCTG ATTTAACAAA	
AATTTAACGC GAATTTTAAC AAAATATTAA	470
CGTTTACAAT TTCATGTACA	

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

AGATCTAATA AGATGATCTT CTTGAGATCG	60
TTTTGGTCTG CGCGTAATCT CTTGCTCTGA	
AAACGAAAAA ACCGCCTTGC AGGGCGGTTT	120
TTCGTAGGTT CTCTGAGCTA CCAACTCTTT	
GAACCGAGGT AACTGGCTTG GAGGAGCGCA	180
GTCACTAAAA CTTGTCCTTT CAGTTTAGCC	
TTAACCGGCG CATGACTTCA AGACTAACTC	240
CTCTAAATCA ATTACCAGTG GCTGCTGCCA	
GTGGTGCTTT TGCATGTCTT TCCGGGTGG	300
ACTCAAGACG ATAGTTACCG GATAAGGCGC	
AGCGGTCGGA CTGAACGGGG GGTTCGTGCA	360
TACAGTCCAG CTTGGAGCGA ACTGCCTACC	
CGGAAGTGA TGTCAGGCGT GGAATGAGAC	420
AAACGCGGCC ATAACAGCGG AATGACACCG	
GTAAACCGAA AGGCAGGAAC AGGAGAGCGC	480
AGGAGGGAGC CGCCAGGGGG AAACGCCTGG	

TATCTTTATA GTCCTGTCGG GTTTCGCCAC CACTGATTTG AGCGTCAGAT TTCGTGATGC 540
 TTGTCAGGGG GCGGAGCCT ATGGAAAAAC GGCTTTGCCG CGGCCCTCTC ACTTCCCTGT 600
 TAAGTATCTT CCTGGCATCT TCCAGGAAAT CTCCGCCCCG TTCGTAAGCC ATTTCCGCTC 660
 GCCGCAGTCG AACGACCGAG CGTAGCGAGT CAGTGAGCGA GGAAGCGGAA TATATCCTGT 720
 ATCATATATT CTGCTGACGC ACCGGTGCAG CCTTTTTTCT CCTGCCACAT GAAGCACTTC 780
 ACTGACACCC TCATCAGTGC CAACATAGTA AGCCAGTATA CACTCCGCTA GC 832

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TTCAGATCT 49

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT GGCACCTTTA 60

CCGTTGCTCT TCACCCCTGT TACCAAAGCC GAATTC 96

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT GGCACCTCTTA 60
 CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG ATGAAGTGCA ATTGGAATTC 120

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

TCTAGAGGTT GAGGTGATTT TATGAAAAG AATATCGCAT TTCTTCTTGC ATCTATGTTT 60
 GTTTTTTCTA TTGCTACAAA TGCATACGCT GAATTC 96

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 79..1158
- (D) OTHER INFORMATION: /product= "lacI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

GCTAGCATCG AATGGCGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT 60
 CAATTCAGGG TGGTGAAT GTG AAA CCA GTA ACG TTA TAC GAT GTC GCA GAG 111
 Val Lys Pro Val Thr Leu Tyr Asp Val Ala Glu
 300 305 310
 TAT GCC GGT GTC TCT TAT CAG ACC GTT TCC CGC GTG GTG AAC CAG GCC 159
 Tyr Ala Gly Val Ser Tyr Gln Thr Val Ser Arg Val Val Asn Gln Ala
 315 320 325
 AGC CAC GTT TCT GCG AAA ACG CGG GAA AAA GTG GAA GCG GCG ATG GCG 207
 Ser His Val Ser Ala Lys Thr Arg Glu Lys Val Glu Ala Ala Met Ala
 330 335 340

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GAG	CTG	AAT	TAC	ATT	CCT	AAC	CGC	GTG	GCA	CAA	CAA	CTG	GCG	GGC	AAA	255
Glu	Leu	Asn	Tyr	Ile	Pro	Asn	Arg	Val	Ala	Gln	Gln	Leu	Ala	Gly	Lys	
		345					350					355				
CAG	TCG	TTG	CTG	ATT	GGC	GTT	GCC	ACC	TCC	AGT	CTG	GCC	CTG	CAC	GCG	303
Gln	Ser	Leu	Leu	Ile	Gly	Val	Ala	Thr	Ser	Ser	Leu	Ala	Leu	His	Ala	
		360				365					370					
CCG	TCG	CAA	ATT	GTC	GCG	GCG	ATT	AAA	TCT	CGC	GCC	GAT	CAA	CTG	GGT	351
Pro	Ser	Gln	Ile	Val	Ala	Ala	Ile	Lys	Ser	Arg	Ala	Asp	Gln	Leu	Gly	
					380					385					390	
GCC	AGC	GTG	GTC	GTG	TCG	ATG	GTA	GAA	CGA	AGC	GGC	GTC	GAA	GCC	TGT	399
Ala	Ser	Val	Val	Val	Ser	Met	Val	Glu	Arg	Ser	Gly	Val	Glu	Ala	Cys	
				395					400					405		
AAA	GCG	GCG	GTG	CAC	AAT	CTT	CTC	GCG	CAA	CGT	GTC	AGT	GGG	CTG	ATT	447
Lys	Ala	Ala	Val	His	Asn	Leu	Leu	Ala	Gln	Arg	Val	Ser	Gly	Leu	Ile	
			410					415					420			
ATT	AAC	TAT	CCG	CTG	GAT	GAC	CAG	GAT	GCT	ATT	GCT	GTG	GAA	GCT	GCC	495
Ile	Asn	Tyr	Pro	Leu	Asp	Asp	Gln	Asp	Ala	Ile	Ala	Val	Glu	Ala	Ala	
		425					430					435				
TGC	ACT	AAT	GTT	CCG	GCG	TTA	TTT	CTT	GAT	GTC	TCT	GAC	CAG	ACA	CCC	543
Cys	Thr	Asn	Val	Pro	Ala	Leu	Phe	Leu	Asp	Val	Ser	Asp	Gln	Thr	Pro	
		440				445					450					
ATC	AAC	AGT	ATT	ATT	TTC	TCC	CAT	GAG	GAC	GGT	ACG	CGA	CTG	GGC	GTG	591
Ile	Asn	Ser	Ile	Ile	Phe	Ser	His	Glu	Asp	Gly	Thr	Arg	Leu	Gly	Val	
					460				465						470	
GAG	CAT	CTG	GTC	GCA	TTG	GGC	CAC	CAG	CAA	ATC	GCG	CTG	TTA	GCT	GGC	639
Glu	His	Leu	Val	Ala	Leu	Gly	His	Gln	Gln	Ile	Ala	Leu	Leu	Ala	Gly	
				475					480					485		
CCA	TTA	AGT	TCT	GTC	TCG	GCG	CGT	CTG	CGT	CTG	GCT	GGC	TGG	CAT	AAA	687
Pro	Leu	Ser	Ser	Val	Ser	Ala	Arg	Leu	Arg	Leu	Ala	Gly	Trp	His	Lys	
			490					495					500			
TAT	CTC	ACT	CGC	AAT	CAA	ATT	CAG	CCG	ATA	GCG	GAA	CGG	GAA	GGC	GAC	735
Tyr	Leu	Thr	Arg	Asn	Gln	Ile	Gln	Pro	Ile	Ala	Glu	Arg	Glu	Gly	Asp	
		505					510					515				
TGG	AGT	GCC	ATG	TCC	GGT	TTT	CAA	CAA	ACC	ATG	CAA	ATG	CTG	AAT	GAG	783
Trp	Ser	Ala	Met	Ser	Gly	Phe	Gln	Gln	Thr	Met	Gln	Met	Leu	Asn	Glu	
		520				525					530					
GGC	ATC	GTT	CCC	ACT	GCG	ATG	CTG	GTT	GCC	AAC	GAT	CAG	ATG	GCG	CTG	831
Gly	Ile	Val	Pro	Thr	Ala	Met	Leu	Val	Ala	Asn	Asp	Gln	Met	Ala	Leu	
					540					545					550	
GGC	GCA	ATG	CGT	GCC	ATT	ACC	GAG	TCC	GGG	CTG	GCG	GTT	GGT	GCG	GAC	879
Gly	Ala	Met	Arg	Ala	Ile	Thr	Glu	Ser	Gly	Leu	Arg	Val	Gly	Ala	Asp	
				555					560					565		
ATC	TCG	GTA	GTG	GGA	TAC	GAC	GAT	ACC	GAG	GAC	AGC	TCA	TGT	TAT	ATC	927
Ile	Ser	Val	Val	Gly	Tyr	Asp	Asp	Thr	Glu	Asp	Ser	Ser	Cys	Tyr	Ile	
			570					575					580			
CCG	CCG	CTG	ACC	ACC	ATC	AAA	CAG	GAT	TTT	GCG	CTG	CTG	GGG	CAA	ACC	975

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Pro	Pro	Leu	Thr	Thr	Ile	Lys	Gln	Asp	Phe	Arg	Leu	Leu	Gly	Gln	Thr		
		585					590					595					
AGC	GTG	GAC	CGC	TTG	CTG	CAA	CTC	TCT	CAG	GGC	CAG	GCG	GTG	AAG	GGC	1023	
Ser	Val	Asp	Arg	Leu	Leu	Gln	Leu	Ser	Gln	Gly	Gln	Ala	Val	Lys	Gly		
	600					605					610						
AAT	CAG	CTG	TTG	CCC	GTC	TCA	CTG	GTG	AAA	AGA	AAA	ACC	ACC	CTG	GCT	1071	
Asn	Gln	Leu	Leu	Pro	Val	Ser	Leu	Val	Lys	Arg	Lys	Thr	Thr	Leu	Ala		
615					620				625					630			
CCC	AAT	ACG	CAA	ACC	GCC	TCT	CCC	CGC	GCG	TTG	GCC	GAT	TCA	CTG	ATG	1119	
Pro	Asn	Thr	Gln	Thr	Ala	Ser	Pro	Arg	Ala	Leu	Ala	Asp	Ser	Leu	Met		
				635					640					645			
CAG	CTG	GCA	CGA	CAG	GTT	TCC	CGA	CTG	GAA	AGC	GGG	CAG	TGAGGCTACC			1168	
Gln	Leu	Ala	Arg	Gln	Val	Ser	Arg	Leu	Glu	Ser	Gly	Gln					
			650					655									
CGATAAAAGC	GGCTTCCTGA	CAGGAGGCCG	TTTTGT	TTTGT												1221	

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Val	Lys	Pro	Val	Thr	Leu	Tyr	Asp	Val	Ala	Glu	Tyr	Ala	Gly	Val	Ser		
1				5					10					15			
Tyr	Gln	Thr	Val	Ser	Arg	Val	Val	Asn	Gln	Ala	Ser	His	Val	Ser	Ala		
		20						25					30				
Lys	Thr	Arg	Glu	Lys	Val	Glu	Ala	Ala	Met	Ala	Glu	Leu	Asn	Tyr	Ile		
		35					40					45					
Pro	Asn	Arg	Val	Ala	Gln	Gln	Leu	Ala	Gly	Lys	Gln	Ser	Leu	Leu	Ile		
	50					55					60						
Gly	Val	Ala	Thr	Ser	Ser	Leu	Ala	Leu	His	Ala	Pro	Ser	Gln	Ile	Val		
65					70					75				80			
Ala	Ala	Ile	Lys	Ser	Arg	Ala	Asp	Gln	Leu	Gly	Ala	Ser	Val	Val	Val		
			85						90					95			
Ser	Met	Val	Glu	Arg	Ser	Gly	Val	Glu	Ala	Cys	Lys	Ala	Ala	Val	His		
		100						105					110				
Asn	Leu	Leu	Ala	Gln	Arg	Val	Ser	Gly	Leu	Ile	Ile	Asn	Tyr	Pro	Leu		
		115					120					125					
Asp	Asp	Gln	Asp	Ala	Ile	Ala	Val	Glu	Ala	Ala	Cys	Thr	Asn	Val	Pro		
	130					135					140						
Ala	Leu	Phe	Leu	Asp	Val	Ser	Asp	Gln	Thr	Pro	Ile	Asn	Ser	Ile	Ile		
145					150					155				160			

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Phe Ser His Glu Asp Gly Thr Arg Leu Gly Val Glu His Leu Val Ala
 165 170 175
 Leu Gly His Gln Gln Ile Ala Leu Leu Ala Gly Pro Leu Ser Ser Val
 180 185 190
 Ser Ala Arg Leu Arg Leu Ala Gly Trp His Lys Tyr Leu Thr Arg Asn
 195 200 205
 Gln Ile Gln Pro Ile Ala Glu Arg Glu Gly Asp Trp Ser Ala Met Ser
 210 215 220
 Gly Phe Gln Gln Thr Met Gln Met Leu Asn Glu Gly Ile Val Pro Thr
 225 230 235 240
 Ala Met Leu Val Ala Asn Asp Gln Met Ala Leu Gly Ala Met Arg Ala
 245 250 255
 Ile Thr Glu Ser Gly Leu Arg Val Gly Ala Asp Ile Ser Val Val Gly
 260 265 270
 Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile Pro Pro Leu Thr Thr
 275 280 285
 Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr Ser Val Asp Arg Leu
 290 295 300
 Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly Asn Gln Leu Leu Pro
 305 310 315 320
 Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala Pro Asn Thr Gln Thr
 325 330 335
 Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met Gln Leu Ala Arg Gln
 340 345 350
 Val Ser Arg Leu Glu Ser Gly Gln
 355 360

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (51..707)
- (D) OTHER INFORMATION: /product= "cat resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT AAAAAAATTA CGCCCCGCC
 TGCCACTCAT CGCAGTACTG TTGTAATTCA TTAAGCATTC TGCCGACATG GAAGCCATCA

60

120

365

CAAACGGCAT GATGAACCTG AATCGCCAGC GGCATCAGCA CCTTGTGCGC TTGCGTATAA	180
TATTTGCCCC TAGTGAAAAC GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA	240
AAACTGGTGA AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC AATAAACCCCT	300
TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT CTTGCGAATA TATGTGTAGA	360
AACTGCCGGA AATCGTCGTG GTATTCACTC CAGAGCGATG AAAACGTTTC AGTTTGCTCA	420
TGGAAAACGG TGTAACAAGG GTGAACACTA TCCCATATCA CCAGCTCACC GTCTTTCATT	480
GCCATACGGA ACTCCGGGTG AGCATTTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA	540
TAAAACTTGT GCTTATTTTT CTTTACGGTC TTTAAAAAGG CCGTAATATC CAGCTGAACG	600
GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT CAAAATGTTT TTTACGATGC	660
CATTGGGATA TATCAACGGT GGTATATCCA GTGATTTTTT TCTCCATTTT AGCTTCCTTA	720
GCTCCTGAAA ATCTCGATAA CTCAAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG	780
TGAAAGTTGG AACCTCACCC GACGTCTAAT GTGAGTTAGC TCACTCATTG GGCACCCCAG	840
GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT	900
CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCTAG ACCCCCCCCC CGCATGCCAT	960
AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA CCTGTGAAGT GAAAAATGGC	1020
GCAGATTGTG CGACATTTTT TTTGTCTGCC GTTTAATTAA AGGGGGGGGG GGGCCGGCCT	1080
GGGGGGGGGT GTACATGAAA TTGTAAACGT TAATATTTTG TTAAAATTTC CGTTAAATTT	1140
TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC CTTATAAATC	1200
AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCAGTT TGGAACAAGA GTCCACTATT	1260
AAAGAACGTG GACTCCAACG TCAAAGGGCG AAAAACCGTC TATCAGGGCG ATGGCCCACT	1320
ACGAGAACCA TCACCCTAAT CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG	1380
GAACCCTAAA GGGAGCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGCGGAG	1440
AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC	1500
GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG CTACAGGGCG CGTGCTAGCG	1560
GAGTGTATAC TGGCTTACTA TGTTGGCACT GATGAGGGTG TCAGTGAAGT GCTTCATGTG	1620
GCAGGAGAAA AAAGGCTGCA CCGGTGCGTC AGCAGAATAT GTGATACAGG ATATATTCCG	1680
CTTCCTCGCT CACTGACTCG CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT	1740
ACGAACGGGG CGGAGATTTT CTGGAAGATG CCAGGAAGAT ACTTAACAGG GAAGTGAGAG	1800
GGCCGCGGCA AAGCCGTTTT TCCATAGGCT CCGCCCCCT GACAAGCATC ACGAAATCTG	1860
ACGCTCAAAT CAGTGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC	1920
TGGCGGCTCC CTCCTGCGCT CTCCTGTTCC TGCCTTTCGG TTTACGGTG TCATTCCGCT	1980

GTTATGGCCG CGTTTGTCTC ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT 2040
 CCAAGCTGGA CTGTATGCAC GAACCCCCCG TTCAGTCCGA CCGCTGCGCC TTATCCGGTA 2100
 ACTATCGTCT TGAGTCCAAC CCGGAAAGAC ATGCAAAAGC ACCACTGGCA GCAGCCACTG 2160
 GTAATTGATT TAGAGGAGTT AGTCTTGAAG TCATGCGCCG GTTAAGGCTA AACTGAAAGG 2220
 ACAAGTTTTA GTGACTGCGC TCCTCCAAGC CAGTTACCTC GGTTCAAAGA GTTGGTAGCT 2280
 CAGAGAACCT ACGAAAAACC GCCCTGCAAG GCGGTTTTTTT CGTTTTCAGA GCAAGAGATT 2340
 ACGCGCAGAC CAAAACGATC TCAAGAAGAT CATCTTATTA 2380

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp
 1 5 10 15
 His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
 20 25 30
 Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
 35 40 45
 Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
 50 55 60
 Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly
 65 70 75 80
 Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His
 85 90 95
 Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp
 100 105 110
 Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly
 115 120 125
 Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe
 130 135 140
 Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
 145 150 155 160
 Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
 165 170 175
 Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
 180 185 190

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His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
 195 200 205

Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
 210 215

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (1341..1997)
- (D) OTHER INFORMATION: /product= "cat resistance"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (2521..3417)
- (D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GTACATGAAA TTGTAAACGT TAATATTTTG TTAAAATTCG CGTTAAATTT TTGTTAAATC	60
AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC CTTATAAATC AAAAGAATAG	120
ACCGAGATAG GGTGAGTGT TGTTCCAGTT TGGAACAAGA GTCCACTATT AAAGAACGTG	180
GACTCCAACG TCAAAGGGCG AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGAGAACCA	240
TCACCCTAAT CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG GAACCCTAA	300
GGGAGCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG	360
AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA	420
ACCACCACAC CCGCCGCGCT TAATGCGCCG CTACAGGGCG CGTGCTAGCG GAGTGTATAC	480
TGGCTTACTA TGTTGGCACT GATGAGGGTG TCAGTGAAGT GCTTCATGTG GCAGGAGAAA	540
AAAGGCTGCA CCGGTGCGTC AGCAGAATAT GTGATACAGG ATATATTCCG CTTCCCTCGCT	600
CACTGACTCG CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT ACGAACGGGG	660
CGGAGATTTT CTGGAAGATG CCAGGAAGAT ACTTAACAGG GAAGTGAGAG GGCCGCGGCA	720
AAGCCGTTTT TCCATAGGCT CCGCCCCCT GACAAGCATC ACGAAATCTG ACGCTCAAAT	780
CAGTGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGCGGCTCC	840
CTCCTGCGCT CTCCTGTTCC TGCCTTTCGG TTTACCGGTG TCATTCCGCT GTTATGGCCG	900
CGTTTGTCTC ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT CCAAGCTGGA	960

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CTGTATGCAC	GAACCCCCCG	TTCAGTCCGA	CCGCTGCGCC	TTATCCGGTA	ACTATCGTCT	1020
TGAGTCCAAC	CCGGAAAGAC	ATGCAAAAGC	ACCACTGGCA	GCAGCCACTG	GTAATTGATT	1080
TAGAGGAGTT	AGTCTTGAAG	TCATGCGCCG	GTTAAGGCTA	AACTGAAAGG	ACAAGTTTTA	1140
GTGACTGCGC	TCCTCCAAGC	CAGTTACCTC	GGTTCAAAGA	GTTGGTAGCT	CAGAGAACCT	1200
ACGAAAAACC	GCCCTGCAAG	GCGGTTTTTT	CGTTTTTCAGA	GCAAGAGATT	ACGCGCAGAC	1260
CAAAACGATC	TCAAGAAGAT	CATCTTATTA	GATCTAGCAC	CAGGCGTTTA	AGGGCACCAA	1320
TAAGTGCCTT	AAAAAAATTA	CGCCCCGCCC	TGCCACTCAT	CGCAGTACTG	TTGTAATTCA	1380
TTAAGCATTC	TGCCGACATG	GAAGCCATCA	CAAACGGCAT	GATGAACCTG	AATCGCCAGC	1440
GGCATCAGCA	CCTTGTGCGC	TTGCGTATAA	TATTTGCCCA	TAGTGAAAAC	GGGGGCGAAG	1500
AAGTTGTCCA	TATTGGCTAC	GTTTAAATCA	AAACTGGTGA	AACTCACCCA	GGGATTGGCT	1560
GAGACGAAAA	ACATATTCTC	AATAAACCCCT	TTAGGGAAAT	AGGCCAGGTT	TTCACCGTAA	1620
CACGCCACAT	CTTGCGAATA	TATGTGTAGA	AACTGCCGGA	AATCGTCGTG	GTATTCACCTC	1680
CAGAGCGATG	AAAACGTTTC	AGTTTGCTCA	TGGAAAACGG	TGTAACAAGG	GTGAACACTA	1740
TCCCATATCA	CCAGCTCACC	GTCTTTTCATT	GCCATACGGA	ACTCCGGGTG	AGCATTCATC	1800
AGGCGGGCAA	GAATGTGAAT	AAAGGCCGGA	TAAAACTTGT	GCTTATTTTT	CTTTACGGTC	1860
TTTAAAAAGG	CCGTAATATC	CAGCTGAACG	GTCTGGTTAT	AGGTACATTG	AGCAACTGAC	1920
TGAAATGCCT	CAAAATGTTT	TTTACGATGC	CATTGGGATA	TATCAACGGT	GGTATATCCA	1980
GTGATTTTTT	TCTCCATTTT	AGCTTCCTTA	GCTCCTGAAA	ATCTCGATAA	CTCAAAAAAT	2040
ACGCCCCGTA	GTGATCTTAT	TTCATTATGG	TGAAAGTTGG	AACCTCACCC	GACGTCTAAT	2100
GTGAGTTAGC	TCACTCATTA	GGCACCCAG	GCTTTTACACT	TTATGCTTCC	GGCTCGTATG	2160
TTGTGTGGAA	TTGTGAGCGG	ATAACAATTT	CACACAGGAA	ACAGCTATGA	CCATGATTAC	2220
GAATTTCTAG	ACCCCCCCCC	CGCATGCCAT	AACTTCGTAT	AATGTACGCT	ATACGAAGTT	2280
ATAAGCTTGA	CCTGTGAAGT	GAAAAATGGC	GCAGATTGTG	CGACATTTTT	TTTGTCTGCC	2340
GTTTAATTAA	GGGGGGGGGC	CGGCCATTAT	CAAAAAGGAT	CTCAAGAAGA	TCCTTTGATC	2400
TTTTCTACGG	GGTCTGACGC	TCAGTGGAAC	GAAAACTCAC	GTTAAGGGAT	TTTGGTCATG	2460
AGATTATCAA	AAAGGATCTT	CACCTAGATC	CTTTTAAATT	AAAAATGAAG	TTTTAAATCA	2520
ATCTAAAGTA	TATATGAGTA	AACTTGGTCT	GACAGTTACC	CAATGCTTAA	TCAGTGAGGC	2580
ACCTATCTCA	GCGATCTGTC	TATTTTCGTT	ATCCATAGTT	GCCTGACTCC	CCGTCGTGTA	2640
GATAACTACG	ATACGGGAGG	GCTTACCATC	TGGCCCCAGT	GCTGCAATGA	TACCGCGAGA	2700
CCCACGCTCA	CCGGCTCCAG	ATTTATCAGC	AATAAACCAG	CCAGCCGGAA	GGGCCGAGCG	2760
CAGAAGTGGT	CCTGCAACTT	TATCCGCCTC	CATCCAGTCT	ATTAAGTGT	GCCGGGAAGC	2820

TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT	2880
CGTGGTGTCA CGCTCGTCGT TTGGTATGGC TTCATTACAGC TCCGGTTCCC AACGATCAAG	2940
GCGAGTTACA TGATCCCCCA TGTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT	3000
CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA	3060
TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG ACTGGTGAGT ACTCAACCAA	3120
GTCATTCTGA GAATAGTGTA TCGGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA	3180
TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAGAAC GTTCTTCGGG	3240
GCGAAAAC TC AAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGCGC	3300
ACCCAAC TGA TCCTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG	3360
AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GCGACACGG AAATGTTGAA TACTCATACT	3420
CTTCCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT	3480
ATTTGAAT	3488

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met	Glu	Lys	Lys	Ile	Thr	Gly	Tyr	Thr	Thr	Val	Asp	Ile	Ser	Gln	Trp
1				5					10					15	
His	Arg	Lys	Glu	His	Phe	Glu	Ala	Phe	Gln	Ser	Val	Ala	Gln	Cys	Thr
			20					25					30		
Tyr	Asn	Gln	Thr	Val	Gln	Leu	Asp	Ile	Thr	Ala	Phe	Leu	Lys	Thr	Val
	35					40						45			
Lys	Lys	Asn	Lys	His	Lys	Phe	Tyr	Pro	Ala	Phe	Ile	His	Ile	Leu	Ala
	50					55					60				
Arg	Leu	Met	Asn	Ala	His	Pro	Glu	Phe	Arg	Met	Ala	Met	Lys	Asp	Gly
65					70				75					80	
Glu	Leu	Val	Ile	Trp	Asp	Ser	Val	His	Pro	Cys	Tyr	Thr	Val	Phe	His
			85					90						95	
Glu	Gln	Thr	Glu	Thr	Phe	Ser	Ser	Leu	Trp	Ser	Glu	Tyr	His	Asp	Asp
		100						105					110		
Phe	Arg	Gln	Phe	Leu	His	Ile	Tyr	Ser	Gln	Asp	Val	Ala	Cys	Tyr	Gly
	115						120					125			
Glu	Asn	Leu	Ala	Tyr	Phe	Pro	Lys	Gly	Phe	Ile	Glu	Asn	Met	Phe	Phe
	130					135					140				

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Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
 145 150 155 160
 Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
 165 170 175
 Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
 180 185 190
 His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
 195 200 205
 Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
 210 215

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15
 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80
 Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190

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Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Val Thr
 275 280 285

Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu Asp
 290 295

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (471..1367)
- (D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GATCTCATAA CTTCGTATAA TGTATGCTAT ACGAAGTTAT GACGTCTAAT GTGAGTTAGC	60
TCACATCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA	120
TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCTAG	180
ACCCCCCCCC CGCATGCCAT AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA	240
CCTGTGAAGT GAAAAATGGC GCAGATTGTG CGACATTTTT TTTGTCTGCC GTTTAATTAA	300
GGGGGGGGGC CGGCCATTAT CAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG	360
GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA	420
AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA ATCTAAAGTA	480
TATATGAGTA AACTTGGTCT GACAGTTACC CAATGCTTAA TCAGTGAGGC ACCTATCTCA	540
GCGATCTGTC TATTTTCGTT ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG	600

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ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA CCCACGCTCA	660
CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT	720
CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAAGTGT GCGGGGAAGC TAGAGTAAGT	780
AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT CGTGGTGTCA	840
CGCTCGTCGT TTGGTATGGC TTCATTACAG TCCGGTTCCT AACGATCAAG GCGAGTTACA	900
TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT CGTTGTGAGA	960
AGTAAGTTGG CCGCAGTGT ATCACTCATG GTTATGGCAG CACTGCATAA TTCTCTTACT	1020
GTCATGCCAT CCGTAAGATG CTTTTCTGTG ACTGGTGAGT ACTCAACCAA GTCATTCTGA	1080
GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA TAATACCGCG	1140
CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACCTC	1200
TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGCGC ACCCAACTGA	1260
TCCTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAACAGG AAGGCAAAAT	1320
GCCGCAAAAA AGGGAATAAG GCGACACGG AAATGTTGAA TACTCATACT CTTCTTTTTT	1380
CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT	1440
ACATGAAATT GTAAACGTTA ATATTTTGTT AAAATTCGCG TTAAATTTTT GTTAAATCAG	1500
CTCATTTTTT AACCAATAGG CCGAAATCGG CAAAATCCCT TATAAATCAA AAGAATAGAC	1560
CGAGATAGGG TTGAGTGTTG TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA	1620
CTCCAACGTC AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GAGAACCATC	1680
ACCCTAATCA AGTTTTTTTG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG	1740
GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA AGGAAGGGAA	1800
GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA GCGGTCACGC TGCGCGTAAC	1860
CACCACACCC GCCGCGCTTA ATGCGCCGCT ACAGGGCGCG TGCTAGCGGA GTGTATACTG	1920
GCTTACTATG TTGGCACTGA TGAGGGTGTC AGTGAAGTGC TTCATGTGGC AGGAGAAAAA	1980
AGGCTGCACC GGTGCGTCAG CAGAATATGT GATACAGGAT ATATTCCGCT TCCTCGCTCA	2040
CTGACTCGCT ACGCTCGGTC GTTCGACTGC GGCGAGCGGA AATGGCTTAC GAACGGGGCG	2100
GAGATTCCTT GGAAGATGCC AGGAAGATAC TTAACAGGGA AGTGAGAGGG CCGCGGCAAA	2160
GCCGTTTTTC CATAGGCTCC GCCCCCTGA CAAGCATCAC GAAATCTGAC GCTCAAATCA	2220
GTGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GCGGCTCCCT	2280
CCTGCGCTCT CCTGTTCTTG CTTTCGGTT TACCGGTGTC ATTCCGCTGT TATGGCCGCG	2340
TTTGTCTCAT TCCACGCTG ACACTCAGTT CCGGGTAGGC AGTTCGCTCC AAGCTGGACT	2400
GTATGCACGA ACCCCCCGTT CAGTCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG	2460

AGTCCAACCC GGAAAGACAT GCAAAAGCAC CACTGGCAGC AGCCACTGGT AATTGATTTA 2520
 GAGGAGTTAG TCTTGAAGTC ATGCGC~~C~~GGT TAAGGCTAAA CTGAAAGGAC AAGTTTTAGT 2580
 GACTGCGCTC CTCCAAGCCA GTTACCTCGG TTCAAAGAGT TGGTAGCTCA GAGAACCTAC 2640
 GAAAAACCGC CCTGCAAGGC GGTTTTTTTCG TTTTCAGAGC AAGAGATTAC GCGCAGACCA 2700
 AAACGATCTC AAGAAGATCA TCTTATTA 2728

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15
 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80
 Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220

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Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Val Thr
 275 280 285

Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu Asp
 290 295

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TATGAGATCT CATAACTTCG TATAATGTAC GCTATACGAA GTTAT

45

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

TAATAACTTC GTATAGCATA CATTATACGA AGTTATGAGA TCTCA

45

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CATTTTTTGC CCTCGTTATC TACGCATGCG ATAAC TTCGT ATAGCGTACA TTATACGAAG 60
 TTATTCTAGA CATGGTCATA GCTGTTTCCT G 91

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GGGGGGAATT CGGTGGTGGT GGATCTGCGT GCGCTGAAAC GGTGAAAGT TG 52

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CCCCCCAAG CTTATCAAGA CTCCTTATTA CG 32

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

376

GGGGGGGGGAA TTCGAGGCG GTTCCGGTGG TGGC

34

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GGGGGGGGGAA TTCGAGCAGA AGCTGATCTC TGAGGAGGAT CTGTAGGGTG GTGGCTCTGG

60

TTCGGGTGAT TTTG

74

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CCATAACTTC GTATAATGTA CGCTATACGA AGTTATA

37

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

AGCTTATAAC TTCGTATAGC GTACATTATA CGAAGTTATG GCATG

45

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs

377

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGCTTGACCT GTGAAGTGAA AAATGGCGCA GATTGTGCGA CATTTTTTTT GTCTGCCGTT 60
 TAATTAAAGG GGGGGT 76

- (2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GTACACCCCC CCCAGGCCG GCCCCCCCCC CCCTTTAATT AAACGGCAGA CAAAAAAAAT 60
 GTCGCACAAT CTGCG 75

- (2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GGGGGGGTGT ACATTCAAAT ATGTATCCGC TCATG 35

- (2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

378

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

GGGTTACATC GAACTGGATC TC

22

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCAGTTCGAT GTAACCCACT CGCGCACCCA ACTGATCCTC AGCATCTTTT ACTTTCACC

59

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

ACTCTAGCTT CCCGGCAACA GTTAATAGAC TGGATGGAGG CGG

43

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

379

CTGTTGCCGG GAAGCTAGAG TAAG

24

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCCCCCTTA ATTAAGGGGG GGGGCCGCC ATTATCAAAA AGGATCTCAA GAAGATCC

58

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GGGGGGGGCT AGCACGCGCC CTGTAGCGGC GCATTAA

37

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CCCCCCTGT ACATGAAATT GTAAACGTTA ATATTTTG

38

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

388

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

GGGCGATGGC CCACTACGAG AACCATCACC CTAATC

36

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GGGGGGAGAT CTAATAAGAT GATCTTCTTG AG

32

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

GAGTTGGTAG CTCAGAGAAC CTACGAAAAA CCGCCCTGCA AGGCG

45

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GTAGGTTCTC TGAGCTACCA ACTC

24

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GTTTCCCCCT GGCGGCTCCC TCCTGCGCTC TCCTGTTCTC GCC

43

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

AGGAGGGAGC CGCCAGGGGG AAAC

24

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACATCAGCG CTAGCGGAGT GTATAC

26

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs

382

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

GATCTCATAA CTTCGTATAA TGTATGCTAT ACGAAGTTAT TCA

43

- (2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GATCTGAATA ACTTCGTATA GCATACATTA TACGAAGTTA TGAGA

45

- (2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GGGGGGGAGA TCTGACCAA ATCCCTTAAC GTGAG

35

- (2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GGTATCTGCG CTCTGCTGTA GCCAGTTACC TTCGG

35

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

CCCCCCCCGCT AGCCATGTGA GCAAAAGGCC AGCAA

35

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GGGACGTCGG GTGAGGTTCC AAC

23

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCATACGGAA CTCCGGGTGA GCATTCATC

29

(2) INFORMATION FOR SEQ ID NO: 334:

384

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCGGAGTTCC GTATGG

16

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

ACGTTTAAAT CAAAACTGG

19

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CCAGTTTTGA TTAAACGTA GCCAATATGG ACAACTTCTT CGCCCCCGTT TTCACTATGG
GCAAATATT

60

69

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

385

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

GGAAGATCTA GCACCAGGCG TTTAAG

26

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GAGGCCGGCC ATCGAATGGC GCAAAAC

27

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CGCGTACCGT CCTCATGGGA GAAAATAATA C

31

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

386

CCATGAGGAC GGTACGCGAC TGGGCGTGGA GCATCTGGTC GCATTGGGTC ACCAGCAAAT 60
 CCGCTGTTAG CTGGCCCATT AAG 83

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GTCAGCGGCG GGATATAACA TGAGCTGTCC TCGGTATCGT CG 42

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GTTATATCCC GCCGCTGACC ACCATCAAAC 30

(2) INFORMATION FOR SEQ ID NO: 343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(42..44, "")
- (D) OTHER INFORMATION: /note= "in Fig.35b, M41, LAC6: T4T;
 but see Fig.35a, M41: LAC6 pos.1055-1119 on complementary
 strand, 1076 to 1078: TAT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

387

CATCACTGAA TCGGCCAACG CGCGGGGAGA GCGGTTTTC GTATTGGGAG CCAGGGTGGT 60
 TTTTC 65

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

GGTTAATTAA CCTCACTGCC CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATCAG 60
 TGAATCGGCC AAC 73

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

CTAGACTAGT GTTTAAACCG GACCGGGGGG GGGCTTAAGG GGGGGGGGGG 50

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CTAGCCCCC CCCCCCTTAA GCCCCCCCCC GGTCCGGTTT AAACACTAGT 50

(2) INFORMATION FOR SEQ ID NO: 347:

388

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CTAGACTAGT GTTTAAACCG GACCGGGGGG GGGCTTAAGG GGGGGGGGGG

50

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CCCCCCTTA AGTGGGCTGC AAAACAAAAC GGCTCCTGT CAGGAAGCCG CTTTTATCGG
GTAGCCTCAC TGCCCGCTTT CC

60

82

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GTTGTTGTGC CACGCGGTTA GGAATGTAAT TCAGCTCCGC

40

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

389

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

AACCGCGTGG CACAACAAC

19

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CTTCGTTCTA CCATCGACAC GACCACGCTG GCACCCAGTT G

41

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

GTGTCGATGG TAGAACGAAG

20

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

390

CCACAGCAAT AGCATCCTGG TCATCCAGCG GATAGTTAAT AATCAGCCCA CTGACACGTT
GCGCGAG

60

67

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GACCAGGATG CTATTGCTGT GG

22

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CAGCGCGATT TGCTGGTGGC CCAATGCGAC CAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

CACCAGCAAA TCGCGCTG

18

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs

391

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

CCCGGACTCG GTAATGGCAC GCATTGCGCC CAGCGCC

37

- (2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GCCATTACCG AGTCCGGG

18

- (2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

AATTCACCA TCATCACCAT TGACGTCTA

29

- (2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

AGCTTAGACG TCAATGGTGA TGATGGTGG

29

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (280..1137)
- (D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CGCGTTAACC TCAGGTGACC AAGCCCCTGG CCAAGGTCCC GTACGTTCTGA AGATTACCAT	60
CACGTGGATC CGGTACCAGG CCGGCCATTA TCAAAAAGGA TCTCAAGAAG ATCCTTTTGAT	120
CTTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAACTCA CGTTAAGGGA TTTTGGTTCAT	180
GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC	240
AATCTAAAGT ATATATGAGT AAACCTGGTC TGACAGTTAC CAATGCTTAA TCAGTGAGGC	300
ACCTATCTCA GCGATCTGTC TATTTTCGTT ATCCATAGTT GCCTGACTCC CCGTCGTGTA	360
GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA	420
CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA GGGCCGAGCG	480
CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAAGTGTG GCCGGGAAGC	540
TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT	600
CGTGGTGTCA CGCTCGTCGT TTGGTATGGC TTCATTACG TCCGGTTCCC AACGATCAAG	660
GCGAGTTACA TGATCCCCCA TGTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT	720
CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA	780
TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTGGTGAGT ACTCAACCAA	840
GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA	900
TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG	960
CGGAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC	1020
ACCCAAGTGA TCTTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAACAGG	1080

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AAGGCAAAAT GCCGCAAAA AGGGAATAAG GGCGACACGG AAATGTTGAA TACTCATACT 1140
 CTTCTTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT 1200
 ATTTGAATGT ACTCGGCCGC ACGAGCTGCA GGCGCCATTA ATGGCTCGAG CGCGCTTCAG 1260
 CGCTTTGTCT TCCGGATGTA CATGAAATT 1289

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15
 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80
 Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220
 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser

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225	230	235	240
Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile			
	245	250	255
Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn			
	260	265	270
Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp			
	275	280	285

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GCCCTGCAAG CGGAAGAC

18

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GGCTTTCGAA TGGCCAAAGG

20

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 25..27

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(D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (ACT/GTT)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:37..39
(D) OTHER INFORMATION:/product= "random codon by trinucleotides (TTT,CAT,CTT,ATG,CAG)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:43..45
(D) OTHER INFORMATION:/product= "random codon by trinucleotides (18 codons, no Pro, no Cys)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:46..48
(D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT, TAT)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:49..51
(D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:52..54
(D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:55..57
(D) OTHER INFORMATION:/product= "random codon by trinucleotides (CCT/TCT)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:58..60
(D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

GCCCTGCAAG CGGAAGACTT TGCGRYTTAT TATTGCHWKC AGNNKDVTDV TNNKYCTNNK
ACCTTTGGCC ATTCGAAAGC C

60

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(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

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library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:37..39
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (TTT,CAT,CTT,ATG,CAG)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:43..45
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (18 codons, no Pro, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:46..48
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:49..51
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:52..54
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:55..57
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CCT/TCT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:58..60
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCCCTGCAAG CGGAAGACGT GGGCGTGTAT TATTGCHWKC AGNNKDVTDV TNNKYCTNNK 60

ACCTTTGGCC ATTCGAAAGC C 81

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

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library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:37..39
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (TTT,CAT,CTT,ATG,CAG)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:43..45
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (18 codons, no Pro, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:46..48
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:49..51
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:52..54
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:55..57
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CCT/TCT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:58..60
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GCCCTGCAAG CGGAAGACGT GCGGGTGTAT TATTGCHWKC AGNNKDVTDV TNNKYCTNNK	60
ACCTTTGGCC ATTCGAAAGC C	81

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

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library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:41..43
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CGT, TGG, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:47..61
- (D) OTHER INFORMATION:/product= "random codons by trinucleotides (18 aa, no Trp, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:62..64
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

CCTGCAAGCG GAAGACGAAG CGGATTATTA TTGCCAGAGC YRKGACNNKN NKNNKNNKNN 60

KNNKGGCGGC GGCACGAAGT TAACCGTTCT TGGCCAGGAA TTCGAGCC 108

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:41..43
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CGT, TGG, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:47..58
- (D) OTHER INFORMATION:/product= "random codons by trinucleotides (18 aa, no Trp, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:59..61
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

399

CCTGCAAGCG GAAGACGAAG CGGATTATTA TTGCCAGAGC YRKGACNNKN NKNNKNNKNN 60

KGGCGGCGGC ACGAAGTTAA CCGTTCTTGG CCAGGAATTC GAGCC 105

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:41..43
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CGT, TGG, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:47..55
- (D) OTHER INFORMATION:/product= "random codons by trinucleotides (18 aa, no Trp, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:56..58
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

CCTGCAAGCG GAAGACGAAG CGGATTATTA TTGCCAGAGC YRKGACNNKN NKNNKNNKGG 60

CGGCGGCACG AAGTTAACCG TTCTTGGCCA GGAATTCGAG CC 102

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GGCTCGAATT CCTGGCC

17

400